

A

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<110> Edinger, Shlomit R
Gerlach, Valerie
MacDougall, John R
Malyankar, Muriel M
Smithson, Glennnda
Millet, Isabelle
Peyman, John A
Stone, David J
Gunther, Erik
Ellerman, Karen
Shimkets, Richard A
Padigaru, Muralidhara
Guo, Xiaojia
Patturajan, Meera
Taupier Jr, Raymond J
Burgess, Catherine E
Zerhusen, Bryan D
Kekuda, Ramesh
Spytek, Kimberly A
Gangolli, Esha A
Fernandes, Elma R
Gorman, Linda

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<212> PRT

<213> Homo sapiens

<400> 6

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Val	Ser	Glu	Val	Glu	Pro	Ala	Phe	Leu	Gln	Val	Cys	Arg	Ala	Arg	Glu
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Leu	Arg	Leu	Cys	Val	Glu	Ala	Phe	Pro	Ile	Ala	Asn	Ser	Gln	Pro	Gly
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Phe	Leu	Asn	Leu	Ser	Asn	Val	Arg	Ser	His	Trp	Arg	Glu	Gln	His	Ala
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85										90					95						
Ser	Lys	Arg	Ile	Ile	Thr	Asn	Ala	Met	Leu	Gly	Glu	Ser	Ala	Leu	Ala						
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Ser	Thr	Arg	Lys	Ser	Asn	Cys	Val	Phe	Phe	Leu	Ser	Phe	Tyr	Phe	Phe						
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Gln	Ser	Gly	Met	Ile	Arg	Thr	Glu	Glu	Ala	Asp	Tyr	Phe	Leu	Arg	Pro						
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Leu	Pro	Ser	His	Leu	Ser	Trp	Lys	Leu	Gly	Arg	Ala	Ala	Gln	Gly	Ser						
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Ser	Pro	Ser	His	Val	Leu	Tyr	Lys	Arg	Glu	Val	Leu	Val	Thr	Ser	Arg						
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Thr	Trp	Glu	Leu	Ala	His	Gln	Pro	Leu	His	Ser	Ser	Asp	Leu	Arg	Leu						
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Pro	Gln	Pro	Pro	Lys	Glu	Asp	Leu	Phe	Ile	Leu	Pro	Asp	Glu	Tyr	Lys						
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Ser	Cys	Leu	Arg	His	Lys	Arg	Ser	Leu	Leu	Arg	Ser	His	Arg	Asn	Glu						
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Glu	Leu	Asn	Val	Glu	Thr	Leu	Val	Val	Val	Asp	Lys	Lys	Met	Met	Gln						
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Asn	His	Gly	His	Glu	Asn	Ile	Thr	Thr	Tyr	Val	Leu	Thr	Ile	Leu	Asn						
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Met	Val	Ser	Ala	Leu	Phe	Lys	Asp	Gly	Thr	Ile	Gly	Gly	Asn	Ile	Asn						
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Ile	Ala	Ile	Val	Gly	Leu	Ile	Leu	Leu	Glu	Asp	Glu	Gln	Pro	Gly	Leu						
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Gln	Ser	Gly	Leu	Met	Gly	Lys	Asp	Gly	Thr	Arg	His	Asp	His	Ala	Ile						
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Leu	Leu	Thr	Gly	Leu	Asp	Ile	Cys	Ser	Trp	Lys	Asn	Glu	Pro	Cys	Asp						
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Thr	Leu	Gly	Phe	Ala	Pro	Ile	Ser	Gly	Met	Cys	Ser	Lys	Tyr	Arg	Ser						
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Cys	Thr	Ile	Asn	Glu	Asp	Thr	Gly	Leu	Gly	Leu	Ala	Phe	Thr	Ile	Ala						
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His	Glu	Ser	Gly	His	Asn	Phe	Gly	Met	Ile	His	Asp	Gly	Glu	Gly	Asn						

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Arg Asn Gly Val Phe Ser Trp Ser Pro Cys Ser Arg Gln Tyr Leu His						
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Lys Phe Leu Ser Thr Ala Gln Ala Ile Cys Leu Ala Asp Gln Pro Lys						
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Pro Val Lys Glu Tyr Lys Tyr Pro Glu Lys Leu Pro Gly Glu Leu Tyr						
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Gly Ala Asn Thr Gln Cys Lys Trp Gln Phe Gly Glu Lys Ala Lys Leu						
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Cys Met Leu Asp Phe Lys Lys Asp Ile Cys Lys Ala Leu Trp Cys His						
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Arg Ile Gly Arg Lys Cys Glu Thr Lys Phe Met Pro Ala Ala Glu Gly						
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Thr Ile Cys Gly His Glu His Gly Ala Gly Gly Gln Cys Val Lys Tyr						
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Gly Asp Glu Gly Pro Lys Pro Thr His Gly His Trp Ser Asp Trp Ser						
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Ser Trp Ser Pro Cys Ser Arg Thr Cys Gly Gly Gly Val Ser His Arg						
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Ser Arg Arg Phe Arg Gly Arg His Tyr Lys Trp Lys Pro Asp Gln Asp						
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Asn Val Cys Ile Asp Gly Ile Cys Glu Arg Val Gly Cys Asp Asn Val						
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Asn Ser Ala Cys Thr Ile His Arg Gly Leu Tyr Leu Glu Tyr Tyr His						

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Tyr Leu Asn Gly His Trp Thr Val Asp Trp Pro Gly Arg Tyr Lys Phe		
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Ser Gly Thr Thr Phe Asp Tyr Arg Arg Ser Tyr Asn Glu Pro Glu Asn		
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Leu Ile Ala Thr Gly Pro Thr Asn Glu Thr Leu Ile Val Glu Leu Leu		
	770	775 780
Phe Gln Gly Arg Asn Pro Gly Val Ala Trp Glu Tyr Ser Met Pro Arg		
785	790	795 800
Leu Gly Thr Glu Lys Gln Pro Pro Ala Gln Pro Ser Tyr Thr Trp Ala		
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Ile Val Arg Ser Glu Cys Ser Val Ser Cys Gly Gly Gly Arg Cys Leu		
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 Ala Gly Thr Cys Val Arg His Gly Thr Arg Ser Gly Ser Ala Trp Glu
 65 70 75 80
 Pro Glu Arg Pro Ala Ser Ser Ser Thr Arg Gly Ala Ala Gly Leu Asp
 85 90 95

Gly Lys Gly Arg Asp Met Asp Glu Ala Gly Asn His Arg Ser Gln Gln
 100 105 110
 Thr Asn Thr Gly Thr Glu Asn Gln Thr Leu His Val Leu Thr Gln Tyr
 115 120 125
 Asp Leu Val Ser Ala Tyr Glu Val Asp His Arg Gly Asp Tyr Val Ser
 130 135 140
 His Glu Ile Met His His Gln Arg Arg Arg Arg Ala Val Ala Val Ser
 145 150 155 160
 Glu Val Glu Ser Leu His Leu Arg Leu Lys Gly Pro Arg His Asp Phe
 165 170 175
 His Met Asp Leu Arg Thr Ser Ser Ser Leu Val Ala Pro Gly Phe Ile
 180 185 190
 Val Gln Thr Leu Gly Lys Thr Gly Thr Lys Ser Val Gln Thr Leu Pro
 195 200 205
 Pro Glu Asp Phe Cys Phe Tyr Gln Gly Ser Leu Arg Ser His Arg Asn
 210 215 220
 Ser Pro Ser His Gly Gly Lys Phe Cys Glu Gly Ser Thr Arg Thr Leu
 225 230 235 240
 Lys Leu Cys Asn Ser Gln Lys Cys Pro Arg Asp Ser Val Asp Phe Arg
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 Ala Ala Gln Cys Ala Glu His Asn Ser Arg Arg Phe Arg Gly Arg His
 260 265 270
 Tyr Lys Trp Lys Pro Tyr Thr Gln Val Glu Ala Asp Leu Cys Lys Leu
 275 280 285
 Tyr Cys Ile Ala Glu Gly Phe Asp Phe Phe Phe Ser Leu Ser Asn Lys
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 Val Lys Asp Gly Thr Pro Cys Ser Glu Asp Ser Arg Asn Val Cys Ile
 305 310 315 320
 Asp Gly Ile Cys Glu Leu Ser Val Val Ser Thr Ser Ala His Met Pro
 325 330 335
 Gln Pro Pro Lys Glu Asp Leu Phe Ile Leu Pro Asp Glu Tyr Lys Ser
 340 345 350
 Cys Leu Arg His Lys Arg Ser Leu Leu Arg Ser His Arg Asn Glu Glu
 355 360 365
 Leu Asn Val Glu Thr Leu Val Val Val Asp Lys Lys Met Met Gln Asn
 370 375 380
 His Gly His Glu Asn Ile Thr Thr Tyr Val Leu Thr Ile Leu Asn Met
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Val Ser Ala Leu Phe Lys Asp Gly Leu Met Gly Lys Asp Gly Thr Arg
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 420 425 430
 Asn Glu Pro Cys Asp Thr Leu Gly Phe Ala Pro Ile Ser Gly Met Cys
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 Ser Lys Tyr Arg Ser Cys Thr Ile Asn Glu Asp Thr Gly Leu Gly Leu
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 Ala Phe Thr Ile Ala His Glu Ser Gly His Asn Phe Gly Met Ile His
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 Asp Gly Glu Gly Asn Met Cys Lys Lys Ser Glu Gly Asn Ile Met Ser
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 Pro Thr Leu Ala Gly Arg Asn Gly Val Phe Ser Trp Ser Pro Cys Ser
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 Arg Gln Tyr Leu His Lys Phe Leu Ser Thr Ala Gln Ala Ile Cys Leu
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 Ala Asp Gln Pro Lys Pro Val Lys Glu Tyr Lys Tyr Pro Glu Lys Leu
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 Pro Gly Glu Leu Tyr Asp Ala Asn Thr Gln Cys Lys Trp Gln Phe Gly
 545 550 555 560
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 565 570 575
 Ala Leu Trp Cys His Arg Ile Gly Arg Lys Cys Glu Thr Lys Phe Met
 580 585 590
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 595 600 605
 Gly Gln Cys Val Lys Tyr Gly Asp Glu Gly Pro Lys Pro Thr His Gly
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 His Trp Ser Asp Trp Ser Ser Trp Ser Pro Cys Ser Arg Thr Cys Gly
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 645 650 655
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Ile Ala Glu Gly Phe Asp Phe Phe Phe Ser Leu Ser Asn Lys Val Lys
725 730 735

Asp Gly Thr Pro Cys Ser Glu Asp Ser Arg Asn Val Cys Ile Asp Gly
740 745 750

Ile Cys Glu Arg Val Gly Cys Asp Asn Val Leu Gly Ser Asp Ala Val
755 760 765

Glu Asp Val Cys Gly Val Cys Asn Gly Asn Asn Ser Ala Cys Thr Ile
770 775 780

His Arg Gly Leu Tyr Thr Lys His His His Thr Asn Gln Tyr Tyr His
785 790 795 800

Met Val Thr Ile Pro Ser Gly Ala Arg Ser Ile Arg Ile Tyr Glu Met
805 810 815

Asn Val Ser Thr Ser Tyr Ile Ser Val Arg Asn Ala Leu Arg Arg Tyr
820 825 830

Tyr Leu Asn Gly His Trp Thr Val Asp Trp Pro Gly Arg Tyr Lys Phe
835 840 845

Ser Gly Thr Thr Phe Asp Tyr Arg Arg Ser Tyr Asn Glu Pro Glu Asn
850 855 860

Leu Ile Ala Thr Gly Pro Thr Asn Glu Thr Leu Ile Val Glu Leu Leu
865 870 875 880

Phe Gln Gly Arg Asn Pro Gly Val Ala Trp Glu Tyr Ser Met Pro Arg
885 890 895

Leu Gly Thr Glu Lys Gln Pro Pro Ala Gln Pro Ser Tyr Thr Trp Ala
900 905 910

Ile Val Arg Ser Glu Cys Ser Val Ser Cys Gly Gly Gly Arg Cys Leu
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Asp Val Lys Phe Thr Val Thr Leu Glu Thr Lys Asp Lys Thr Gln Lys
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Leu Leu Glu Tyr Ser Gly Leu Lys Lys Arg His Leu His Cys Ile Ser
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Phe Leu Val Pro Pro Pro Ala Gly Gly Thr Glu Glu Val Ala Thr Ile
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Arg Val Ser Gly Val Gly Asn Asn Ile Ser Phe Glu Glu Lys Lys Lys
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Pro Leu Tyr Thr Pro Gly Gln Gln Val Tyr Phe Arg Ile Val Thr Met
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Asp Ser Asn Phe Val Pro Val Asn Asp Lys Tyr Ser Met Val Glu Leu
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Gln Asp Pro Asn Ser Asn Arg Ile Ala Gln Trp Leu Glu Val Val Pro
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 Ser Val Leu Pro Lys Phe Lys Val Glu Val Val Glu Pro Lys Glu Leu
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 Ser Gly Lys Met Leu Leu Lys Phe Pro Gln Gly Gly Val Leu Pro Cys
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 Glu Thr Ser Gly Trp Asn Gly Thr Asp Val Ser Leu Glu Gly Lys Phe
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 Gln Met Glu Asp Leu Val Tyr Asn Pro Glu Gln Val Pro Arg Tyr Tyr
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 Gln Asn Ala Tyr Leu His Leu Arg Pro Phe Tyr Ser Thr Thr Arg Ser
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 Phe Leu Gly Ile His Arg Leu Asn Gly Pro Leu Lys Cys Gly Gln Pro
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Gln Glu Val Leu Val Asp Tyr Tyr Ile Asp Pro Ala Asp Ala Ser Pro
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 Gly Ser Lys Asp Leu Gln Asn Val Asn Leu Thr Leu Arg Ile Ile Phe
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 Arg Pro Val Ala Ser Gln Leu Pro His Ile Phe Thr Ser Ser Gly Glu
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 Ser Val Val Ala Arg Phe Glu Ala Gly Glu Leu Ile Thr Gln Arg Glu

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Phe Gly Leu Ile Leu Asp Asp Val Ser Leu Thr Tyr Leu Thr Phe Gly		
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Lys Glu Phe Ile Glu Ala Val Glu Ala Lys Gln Ile Ala Gln Gln Glu		
	180	185 190
Ala Glu Arg Ala Arg Phe Val Val Glu Lys Ala Glu Gln Gln Lys Lys		
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gatcacaagt acacgcccac tctccggaat ggcctggaag agaacttctg ccgtaaccct 480
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cggtcagcaa gacccgcaag ggtgtccagt gccagcgtg gtccgctgag acgccgcaca 1200
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<210> 16

<211> 666

<212> PRT

<213> Homo sapiens

<400> 16

Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Thr Gln Cys Leu Gly Val
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Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr
 20 25 30

Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu
 35 40 45

Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met
 50 55 60

Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu
 65 70 75 80

Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly
 85 90 95

Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met
 100 105 110

Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly Gly
 115 120 125

Leu Pro Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Lys Tyr
 130 135 140

Thr Pro Thr Leu Arg Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn Pro
 145 150 155 160

Asp Gly Asp Pro Gly Gly Pro Trp Cys Tyr Thr Thr Asp Pro Ala Val
 165 170 175

Arg Phe Gln Ser Cys Gly Ile Lys Ser Cys Arg Glu Ala Ala Cys Val
 180 185 190

Trp Cys Asn Gly Glu Glu Tyr Arg Gly Ala Val Asp Arg Thr Glu Ser
 195 200 205
 Gly Arg Glu Cys Gln Arg Trp Asp Leu Gln His Pro His Gln His Pro
 210 215 220
 Phe Glu Pro Gly Lys Phe Leu Asp Gln Gly Leu Asp Asp Asn Tyr Cys
 225 230 235 240
 Arg Asn Pro Asp Gly Ser Glu Arg Pro Trp Cys Tyr Thr Thr Asp Pro
 245 250 255
 Gln Ile Glu Arg Glu Phe Cys Asp Leu Pro Arg Cys Gly Ser Glu Ala
 260 265 270
 Gln Pro Arg Gln Glu Ala Thr Thr Val Ser Cys Phe Arg Gly Lys Gly
 275 280 285
 Glu Gly Tyr Arg Gly Thr Ala Asn Thr Thr Thr Ala Gly Val Pro Cys
 290 295 300
 Gln Arg Trp Asp Ala Gln Ile Pro His Gln His Arg Phe Thr Pro Glu
 305 310 315 320
 Lys Tyr Ala Cys Lys Asp Leu Arg Glu Asn Phe Cys Arg Asn Pro Asp
 325 330 335
 Gly Ser Glu Ala Pro Trp Cys Phe Thr Leu Arg Pro Gly Met Arg Ala
 340 345 350
 Ala Phe Cys Tyr Gln Ile Arg Arg Cys Thr Asp Asp Val Arg Pro Gln
 355 360 365
 Thr Ala Thr Thr Ala Gln Gly Ser Ser Thr Ala Ala Arg Ser Ala Arg
 370 375 380
 Pro Ala Arg Val Ser Ser Ala Ser Ala Gly Pro Leu Arg Arg Arg Thr
 385 390 395 400
 Ser Arg Ser Ser Arg Leu Pro Pro Asn Arg Met His Asn Trp Arg Arg
 405 410 415
 Thr Ser Ala Gly Thr Gln Met Gly Ile Ala Met Gly Pro Gly Ala Thr
 420 425 430
 Arg Trp Thr Gln Gly Pro His Ser Thr Thr Val Pro Cys Asp Ala Ala
 435 440 445
 Leu Met Thr Ser Arg His Gln Ser Trp Thr Pro Gln Thr Arg Cys Ser
 450 455 460
 Leu Arg Ser Val Ala Arg Gly Trp Ile Gly Trp Ile Ser Gly Val Pro
 465 470 475 480
 Ser Cys Ala Trp Leu Gly Ala Ile Arg Ala Thr His Pro Gly Gln Ser
 485 490 495

Ala Cys Gly Ile Gly Met Leu Pro Leu Thr Gly Tyr Glu Val Trp Leu
500 505 510

Gly Thr Leu Phe Gln Asn Pro Gln His Gly Glu Pro Ser Leu Gln Arg
515 520 525

Val Pro Val Ala Lys Met Val Cys Gly Pro Ser Gly Ser Gln Leu Val
530 535 540

Leu Leu Lys Leu Glu Arg Ser Val Thr Leu Asn Gln Arg Val Ala Leu
545 550 555 560

Ile Cys Leu Pro Pro Glu Trp Tyr Val Val Pro Pro Gly Thr Lys Cys
565 570 575

Glu Ile Ala Gly Trp Gly Glu Thr Lys Gly Thr Gly Asn Asp Thr Val
580 585 590

Leu Asn Val Ala Leu Leu Asn Val Ile Ser Asn Gln Glu Cys Asn Ile
595 600 605

Lys His Arg Gly Arg Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr
610 615 620

His Asn Cys Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys
625 630 635 640

Ala Arg Ser Cys Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val
645 650 655

Asp Trp Ile His Lys Val Met Arg Leu Gly
660 665

<210> 17
<211> 634
<212> DNA
<213> Homo sapiens

<400> 17
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tacatgaagg agggaggagt gggaaactgct ttgcgaaaaa tggacgcaat ggccaagcca 180
gattgtatca tcacttgtga tggcaaaaac ctcaccataa aaaccgagag cactttgaaa 240
acacagtttt cttgtaccct gggagagaag tttgaagaaa ccacagctga tggcagaaaa 300
actcagactg tgtgcagctt tgcagatggg gcattgggttc agcatcagga gtgggatggg 360
aaggaaaaca caataacaag aaaactgaaa gatgggaaat tagtgggtgta ctgtgtcatg 420
aacaatgtcg cctgtactcg gatctatgaa aaagtagaat aaaaattcca tcatcacttt 480
ggacaggagt taactaatag aatgatcaag ctacagttcaa tgagcaaate tccatagtgt 540
tttttttcat tactgtgttc aattatcttt atcacaaaacg tttcacatgc agctatttca 600
aagtgtcttg gattaattag gatcatccct ttgg 634

<210> 18
<211> 134
<212> PRT
<213> Homo sapiens

<400> 18

Met Ala Thr Val Gln Gln Leu Gly Gly Arg Trp Arg Leu Val Asp Ser
1 5 10 15

Lys Arg Phe Asp Glu Tyr Met Lys Glu Gly Gly Val Gly Thr Ala Leu
20 25 30

Arg Lys Met Asp Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp
35 40 45

Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Gln Phe
50 55 60

Ser Cys Thr Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly Arg
65 70 75 80

Lys Thr Gln Thr Val Cys Ser Phe Ala Asp Gly Ala Leu Val Gln His
85 90 95

Gln Glu Trp Asp Gly Lys Glu Asn Thr Ile Thr Arg Lys Leu Lys Asp
100 105 110

Gly Lys Leu Val Val Tyr Cys Val Met Asn Asn Val Ala Cys Thr Arg
115 120 125

Ile Tyr Glu Lys Val Glu
130

<210> 19

<211> 822

<212> DNA

<213> Homo sapiens

<400> 19

catgaactgg gcatttctgc agggcctgct gaggggcgtg aacaagtact ccacagtgct 60
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ggaggaggtg tgggacgatg agcagaagga ctttgtctgc aacaccaagc agcccggctg 180
ccccaacgtc tgctatgacg agttcttccc cgtgtccac gtgcgcctct gggccctaca 240
gtcctcctg gtcacgtgcc cctcactgct cgtggtcac cactggcct accgcgagga 300
acgcgagcgc aagcaccacc tgaaacacgg gcccaatgcc ccgtccctgt acgacaacct 360
gagcaagaag cggggcggac tgtggtggac gtacttgctg agcctcatct tcaaggccgc 420
cgtggatgct ggcttctct atattctcca ccgcctctac aaggattatg acatgccccg 480
cgtggtggcc tgctccgtgg agccttgccc ccacactgtg gactgttaca tctcccgccc 540
caggagaag aaggcttcca cctacttcat ggtgaccaca gctgccatct gcctcctgct 600
caacctcagt gaagtcttct acctggtggg caagaggtgc atggagatct tcggccccag 660
gcaccggcgg cctcgggtgcc gggaatgcct acccgatacg tgcccaccat atgtcctctc 720
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ggatgcaggt gggtatccat aacctgcgag atcagcagat aa 822

<210> 20

<211> 266

<212> PRT

<213> Homo sapiens

<400> 20

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Ser Thr Val Leu Ser Arg Ile Trp Leu Ser Val Val Phe Ile Phe Arg
20 25 30
Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Glu Gln
35 40 45
Lys Asp Phe Val Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys
50 55 60
Tyr Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
65 70 75 80
Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
85 90 95
Tyr Arg Glu Glu Arg Glu Arg Lys His His Leu Lys His Gly Pro Asn
100 105 110
Ala Pro Ser Leu Tyr Asp Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp
115 120 125
Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ala Gly
130 135 140
Phe Leu Tyr Ile Phe His Arg Leu Tyr Lys Asp Tyr Asp Met Pro Arg
145 150 155 160
Val Val Ala Cys Ser Val Glu Pro Cys Pro His Thr Val Asp Cys Tyr
165 170 175
Ile Ser Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Thr
180 185 190
Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Ser Glu Val Phe Tyr Leu
195 200 205
Val Gly Lys Arg Cys Met Glu Ile Phe Gly Pro Arg His Arg Arg Pro
210 215 220
Arg Cys Arg Glu Cys Leu Pro Asp Thr Cys Pro Pro Tyr Val Leu Ser
225 230 235 240
Gln Gly Gly His Pro Glu Asp Gly Asn Ser Val Leu Met Lys Ala Gly
245 250 255
Ser Ala Pro Val Asp Ala Gly Gly Tyr Pro
260 265

<210> 21

<211> 546

<212> DNA

<213> Homo sapiens

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<400> 21
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tgtgaactaa atccacagcc acataataat caaaacagaa aagcaaaaaga aagccacttc 180
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ctgcccgggc caccaatctg ttggttcaca ttactacgtg agcaatgtaa gtgtttgcaa 300
gaagccatcc actatctaaa tatcagatat agatgctcca aagcagctac gtcagtgatg 360
agaacagaga aaatacgtag caacatttca ttaagttgaa ttctaatact taaaaggctc 420
cttttagtac tgacattctg gattttaaaa gttatgttga ccgcatgttc tcaactcaca 480
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tgtcag
546

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<210> 22
<211> 61
<212> PRT
<213> Homo sapiens

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<400> 22
Met Leu Gln Ile Ile Glu Asn Met Leu Leu Pro Gly Pro Pro Ile Cys
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Trp Phe Thr Leu Leu Arg Glu Gln Cys Lys Cys Leu Gln Glu Ala Ile
      20             25             30

His Tyr Leu Asn Ile Arg Tyr Arg Cys Ser Lys Ala Ala Thr Ser Val
      35             40             45

Met Arg Thr Glu Lys Ile Arg Ser Asn Ile Ser Leu Ser
      50             55             60

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<210> 23
<211> 2309
<212> DNA
<213> Homo sapiens

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<220>
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<222> (2196)
<223> Wherein n is an a o t o r c o r g.

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<400> 23
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acaagcatat acaatgggga attgacttct tggaaagata tgccaaattt gttaaagaga 180
ggatagaaat tgaacagaac tatgcgaaac aattgagaaa tctggttaag aagtactgcc 240
ccaaacgttc atccaaagat gaagagccac ggtttacctc gtgtgtagcc ttttttaata 300
tccttaatga gttaaattgac tatgcaggac agcgagaagt tgtagcagaa gaaatggcgc 360
acagagtgtg ttgtgaatta atgagatatg ctcatgatct gaaaactgaa agaaaaatgc 420
atctgcaaga aggacgaaaa gctcaacaat atcttgacat gtgctggaaa cagatgggta 480
atagtaaaaa gaagtttgaa agagaatgta gagaggcaga aaaggcacaa cagagttatg 540
aaagattgga taatgatact aatgcaacca aggcagatgt tgaatatgcc aaacagcagt 600
tgaatctgcg tacgcatatg gccgatgaaa ataaaaatgc atatgctgca caattacaaa 660
actttaatgg agaacaacat aaacattttt atgtagtgtat tcctcagatt tacaagcaac 720
tacaagaaat ggacgaacga aggactatta aactcagtga gtgttacaga ggatttgctg 780

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actcagaacg caaagttatt cccatcattt caaaatgttt ggaaggaatg attcttgcag 840
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 ttgaacctcc aggagacttt ccatttgaag attacagtca acatatatat agaaccattt 960
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 aagatttcag tcattctgcca ccagaacaga gacgtaaaaa actacagcag cgcattgatg 1140
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<210> 24

<211> 547

<212> PRT

<213> Homo sapiens

<400> 24

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1

5

10

15

His Thr Gln Trp Gly Ile Asp Phe Leu Glu Arg Tyr Ala Lys Phe Val

20

25

30

Lys Glu Arg Ile Glu Ile Glu Gln Asn Tyr Ala Lys Gln Leu Arg Asn

35

40

45

Leu Val Lys Lys Tyr Cys Pro Lys Arg Ser Ser Lys Asp Glu Glu Pro

50

55

60

Arg Phe Thr Ser Cys Val Ala Phe Phe Asn Ile Leu Asn Glu Leu Asn

65

70

75

80

Asp Tyr Ala Gly Gln Arg Glu Val Val Ala Glu Glu Met Ala His Arg

85

90

95

Val Tyr Gly Glu Leu Met Arg Tyr Ala His Asp Leu Lys Thr Glu Arg

100

105

110

Lys Met His Leu Gln Glu Gly Arg Lys Ala Gln Gln Tyr Leu Asp Met

115

120

125

Cys	Trp	Lys	Gln	Met	Gly	Asn	Ser	Lys	Lys	Lys	Phe	Glu	Arg	Glu	Cys	130	135	140
Arg	Glu	Ala	Glu	Lys	Ala	Gln	Gln	Ser	Tyr	Glu	Arg	Leu	Asp	Asn	Asp	145	150	155
Thr	Asn	Ala	Thr	Lys	Ala	Asp	Val	Glu	Asn	Ala	Lys	Gln	Gln	Leu	Asn	165	170	175
Leu	Arg	Thr	His	Met	Ala	Asp	Glu	Asn	Lys	Asn	Ala	Tyr	Ala	Ala	Gln	180	185	190
Leu	Gln	Asn	Phe	Asn	Gly	Glu	Gln	His	Lys	His	Phe	Tyr	Val	Val	Ile	195	200	205
Pro	Gln	Ile	Tyr	Lys	Gln	Leu	Gln	Glu	Met	Asp	Glu	Arg	Arg	Thr	Ile	210	215	220
Lys	Leu	Ser	Glu	Cys	Tyr	Arg	Gly	Phe	Ala	Asp	Ser	Glu	Arg	Lys	Val	225	230	235
Ile	Pro	Ile	Ile	Ser	Lys	Cys	Leu	Glu	Gly	Met	Ile	Leu	Ala	Ala	Lys	245	250	255
Ser	Val	Asp	Glu	Arg	Arg	Asp	Ser	Gln	Met	Val	Val	Asp	Ser	Phe	Lys	260	265	270
Ser	Gly	Phe	Glu	Pro	Pro	Gly	Asp	Phe	Pro	Phe	Glu	Asp	Tyr	Ser	Gln	275	280	285
His	Ile	Tyr	Arg	Thr	Ile	Ser	Asp	Gly	Thr	Ile	Ser	Ala	Ser	Lys	Gln	290	295	300
Glu	Ser	Gly	Lys	Met	Asp	Ala	Lys	Thr	Pro	Val	Gly	Lys	Ala	Lys	Gly	305	310	315
Lys	Leu	Trp	Leu	Phe	Gly	Lys	Lys	Pro	Lys	Gly	Pro	Ala	Leu	Glu	Asp	325	330	335
Phe	Ser	His	Leu	Pro	Pro	Glu	Gln	Arg	Arg	Lys	Lys	Leu	Gln	Gln	Arg	340	345	350
Ile	Asp	Glu	Leu	Asn	Arg	Glu	Leu	Gln	Lys	Glu	Ser	Asp	Gln	Lys	Asp	355	360	365
Ala	Leu	Asn	Lys	Met	Lys	Asp	Val	Tyr	Glu	Lys	Asp	Pro	Gln	Met	Gly	370	375	380
Asp	Pro	Gly	Ser	Leu	Gln	Pro	Lys	Leu	Ala	Glu	Thr	Met	Asn	Asn	Ile	385	390	395
Asp	Arg	Leu	Arg	Met	Glu	Ile	His	Lys	Asn	Glu	Ala	Trp	Leu	Ser	Glu	405	410	415
Val	Glu	Gly	Lys	Thr	Gly	Gly	Arg	Gly	Asp	Arg	Arg	His	Ser	Ser	Asp	420	425	430

Ile Asn His Leu Val Thr Gln Gly Arg Glu Ser Pro Glu Gly Ser Tyr
 435 440 445

Thr Asp Asp Ala Asn Gln Glu Val Arg Gly Pro Pro Gln Gln His Gly
 450 455 460

His His Asn Glu Phe Asp Asp Glu Phe Glu Asp Asp Asp Pro Leu Pro
 465 470 475 480

Ala Ile Gly His Cys Lys Ala Ile Tyr Pro Phe Asp Gly His Asn Glu
 485 490 495

Gly Thr Leu Ala Met Lys Glu Gly Glu Val Leu Tyr Ile Ile Glu Glu
 500 505 510

Asp Lys Gly Asp Gly Trp Thr Arg Ala Arg Arg Gln Asn Gly Glu Glu
 515 520 525

Gly Tyr Val Pro Thr Ser Tyr Ile Asp Val Thr Leu Glu Lys Asn Ser
 530 535 540

Lys Gly Ser
 545

<210> 25
 <211> 1787
 <212> DNA
 <213> Homo sapiens

<400> 25
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 ggatcttcag agcagagcct ggagaccagc agcatcccat ttctcaggcg gtgtgctggc 180
 gttccatgcg acgtggctgt gcagtgtctg gagccctggg gctgctggcc ggtgcagggtg 240
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 ccttgacagga tgaggagata actttgagct gctcagaggc cagcgtgag gaagctctgc 360
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 cgcaagttag ggatcagcca cgctggctcc tgggtctgcca tgagggtctg agccccgcc 480
 tggggctgca gatctgtctg agccttgggc atctcagact cactcaccac aaggagtaga 540
 acctactga catcaaaact aacagttccc aggagtttgc tcagctctct cctagactgg 600
 gaggttctc ggaggaggcg tggcagccca gtaggactac tgaggctgtt aggaacaact 660
 gcacttctgg tcaagtgtt tccctcagat gctctgagtg tggagcgagg cccctggctt 720
 cccgatagt tgggtggcag tctgtggctc ctgggcgctg gccgtggcag gccagcgtgg 780
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 tgggggcagg agtagggcag ggagatttct aaaggacctg cctcgaatg caaggaacct 1500

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gatgaactgg	gtaagagtat	gcctgagttt	gtatcccaga	tctaccattt	cctgtgtcga	1680
cctttggcaa	atttctaact	ttgttaaacc	ttaatttctt	gataataacc	atgatggcta	1740
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<210> 26
 <211> 1787
 <212> DNA
 <213> Homo sapiens

<400> 26						
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gcacactagg	gggccccgc	tatctccctg	gcatgcatca	gcccctccgt	ccaggtagcc	540
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<210> 27
 <211> 472
 <212> PRT
 <213> Homo sapiens

<400> 27															
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Glu	Glu	Gly	Pro	Gly	Pro	Gly	Ile	Phe	Arg	Ala	Glu	Pro	Gly	Asp	Gln
			20					25					30		

Gln His Pro Ile Ser Gln Ala Val Cys Trp Arg Ser Met Arg Arg Gly
 35 40 45
 Cys Ala Val Leu Gly Ala Leu Gly Leu Leu Ala Gly Ala Gly Val Gly
 50 55 60
 Ser Trp Leu Leu Val Leu Tyr Leu Cys Pro Ala Ala Ser Gln Pro Ile
 65 70 75 80
 Ser Gly Thr Leu Gln Asp Glu Glu Ile Thr Leu Ser Cys Ser Glu Ala
 85 90 95
 Ser Ala Glu Glu Ala Leu Leu Pro Ala Leu Pro Lys Thr Val Ser Phe
 100 105 110
 Arg Ile Asn Ser Glu Asp Phe Leu Leu Glu Ala Gln Val Arg Asp Gln
 115 120 125
 Pro Arg Trp Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu Gly
 130 135 140
 Leu Gln Ile Cys Trp Ser Leu Gly His Leu Arg Leu Thr His His Lys
 145 150 155 160
 Gly Val Asn Leu Thr Asp Ile Lys Leu Asn Ser Ser Gln Glu Phe Ala
 165 170 175
 Gln Leu Ser Pro Arg Leu Gly Gly Phe Leu Glu Glu Ala Trp Gln Pro
 180 185 190
 Ser Arg Thr Thr Glu Ala Val Arg Asn Asn Cys Thr Ser Gly Gln Val
 195 200 205
 Val Ser Leu Arg Cys Ser Glu Cys Gly Ala Arg Pro Leu Ala Ser Arg
 210 215 220
 Ile Val Gly Gly Gln Ser Val Ala Pro Gly Arg Trp Pro Trp Gln Ala
 225 230 235 240
 Ser Val Ala Leu Gly Phe Arg His Thr Cys Gly Gly Ser Val Leu Ala
 245 250 255
 Pro Arg Trp Val Val Thr Ala Ala His Cys Met His Ser Phe Arg Leu
 260 265 270
 Ala Arg Leu Ser Ser Trp Arg Val His Ala Gly Leu Val Ser His Ser
 275 280 285
 Ala Val Arg Pro His Gln Gly Ala Leu Val Glu Arg Ile Ile Pro His
 290 295 300
 Pro Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp Val Ala Leu Leu Arg
 305 310 315 320
 Leu Gln Thr Ala Leu Asn Phe Ser Asp Thr Val Gly Ala Val Cys Leu
 325 330 335

Pro Ala Lys Glu Gln His Phe Pro Lys Gly Ser Arg Cys Trp Val Ser
 340 345 350

Gly Trp Gly His Thr His Pro Ser His Thr Tyr Ser Ser Asp Met Leu
 355 360 365

Gln Asp Thr Val Val Pro Leu Leu Ser Thr Gln Leu Cys Asn Ser Ser
 370 375 380

Cys Val Tyr Ser Gly Ala Leu Thr Pro Arg Met Leu Cys Ala Gly Tyr
 385 390 395 400

Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu
 405 410 415

Val Cys Pro Asp Gly Asp Thr Trp Arg Leu Val Gly Val Val Ser Trp
 420 425 430

Gly Arg Gly Cys Ala Glu Pro Asn His Pro Gly Val Tyr Ala Lys Val
 435 440 445

Ala Glu Phe Leu Asp Trp Ile His Asp Thr Ala Gln Val Ser Val Gly
 450 455 460

Ala Gly Val Gly Gln Gly Asp Phe
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<210> 28

<211> 2148

<212> DNA

<213> Homo sapiens

<400> 28

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gacctgagg ctttacaaca gtgctactga cccctatgag cctgatgctg gatgaccaac 180
cccctatgga ggcccagtat gcagaggagg gcccaggacc tgggatcttc agagcagagc 240
ctggagacca gcagcatccc atttctcagg cgggtgtgctg gcgttccatg cgacgtggct 300
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cagtatcttt cagaataaac agcgaagact tcttgctgga agcgcaagtg agggatcagc 540
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gtgactggga ggtgcccccc gtcccacctt tttcctgtgc tctaggtggg ctaagtgcct 1860
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gagttggtct aggacattgg ttttaaatga cagttctgtg aactggtcca aggaggttct 2100
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<210> 29

<211> 418

<212> PRT

<213> Homo sapiens

<400> 29

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Met Ser Leu Met Leu Asp Asp Gln Pro Pro Met Glu Ala Gln Tyr Ala
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```

```

Glu Glu Gly Pro Gly Pro Gly Ile Phe Arg Ala Glu Pro Gly Asp Gln
      20              25              30

```

```

Gln His Pro Ile Ser Gln Ala Val Cys Trp Arg Ser Met Arg Arg Gly
      35              40              45

```

```

Cys Ala Val Leu Gly Ala Leu Gly Leu Leu Ala Gly Ala Gly Val Gly
      50              55              60

```

```

Ser Trp Leu Leu Val Leu Tyr Leu Cys Pro Ala Ala Ser Gln Pro Ile
      65              70              75              80

```

```

Ser Gly Thr Leu Gln Asp Glu Glu Ile Thr Leu Ser Cys Ser Glu Ala
      85              90              95

```

```

Ser Ala Glu Glu Ala Leu Leu Pro Ala Leu Pro Lys Thr Val Ser Phe
      100             105             110

```

```

Arg Ile Asn Ser Glu Asp Phe Leu Leu Glu Ala Gln Val Arg Asp Gln
      115             120             125

```

```

Pro Arg Trp Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu Gly
      130             135             140

```

```

Leu Gln Ile Cys Trp Ser Leu Gly His Leu Arg Leu Thr His His Lys
      145             150             155             160

```

```

Gly Val Asn Leu Thr Asp Ile Lys Leu Asn Ser Ser Gln Glu Phe Ala
      165             170             175

```

```

Gln Leu Ser Pro Arg Leu Gly Gly Phe Leu Glu Glu Ala Trp Gln Pro
      180             185             190

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Arg Asn Asn Cys Thr Ser Gly Gln Val Val Ser Leu Arg Cys Ser Glu
 195 200 205

Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ser Val
 210 215 220

Ala Pro Gly Arg Trp Pro Trp Gln Ala Ser Val Ala Leu Gly Phe Arg
 225 230 235 240

His Thr Cys Gly Gly Ser Val Leu Ala Pro Arg Trp Val Val Thr Ala
 245 250 255

Ala His Cys Met His Ser Ala Gln Asn His Asp Tyr Asp Val Ala Leu
 260 265 270

Leu Arg Leu Gln Thr Ala Leu Asn Phe Ser Asp Thr Val Gly Ala Val
 275 280 285

Cys Leu Pro Ala Lys Glu Gln His Phe Pro Lys Gly Ser Arg Cys Trp
 290 295 300

Val Ser Gly Trp Cys His Thr His Pro Ser His Thr Tyr Ser Ser Asp
 305 310 315 320

Met Leu Gln Asp Thr Val Val Pro Leu Leu Ser Thr Gln Leu Cys Asn
 325 330 335

Ser Ser Cys Val Tyr Ser Gly Ala Leu Thr Pro Arg Met Leu Cys Ala
 340 345 350

Gly Tyr Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly Gly
 355 360 365

Pro Leu Val Cys Pro Asp Gly Asp Thr Trp Arg Leu Val Gly Val Val
 370 375 380

Ser Trp Gly Arg Gly Cys Ala Glu Pro Asn His Pro Gly Val Tyr Ala
 385 390 395 400

Lys Val Ala Glu Phe Leu Asp Trp Ile His Asp Thr Ala Gln Asp Ser
 405 410 415

Leu Leu

<210> 30

<211> 1593

<212> PRT

<213> Homo sapiens

<400> 30

Met Pro Cys Ala Gln Arg Ser Trp Leu Ala Asn Leu Ser Val Val Ala
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Gln Leu Leu Asn Phe Gly Ala Leu Cys Tyr Gly Arg Gln Pro Gln Pro
 20 25 30

Gly Pro Val Arg Phe Pro Asp Arg Arg Gln Glu His Phe Ile Lys Gly
 35 40 45
 Leu Pro Glu Tyr His Val Val Gly Pro Val Arg Val Asp Ala Ser Gly
 50 55 60
 His Phe Leu Ser Tyr Gly Leu His Tyr Pro Ile Thr Ser Ser Arg Arg
 65 70 75 80
 Lys Arg Asp Leu Asp Gly Ser Glu Asp Trp Val Tyr Tyr Arg Ile Ser
 85 90 95
 His Glu Glu Lys Asp Leu Phe Phe Asn Leu Thr Val Asn Gln Gly Phe
 100 105 110
 Leu Ser Asn Ser Tyr Ile Met Glu Lys Arg Tyr Gly Asn Leu Ser His
 115 120 125
 Val Lys Met Met Ala Ser Ser Ala Pro Leu Cys His Leu Ser Gly Thr
 130 135 140
 Val Leu Gln Gln Gly Thr Arg Val Gly Thr Ala Ala Leu Ser Ala Cys
 145 150 155 160
 His Gly Leu Thr Gly Phe Phe Gln Leu Pro His Gly Asp Phe Phe Ile
 165 170 175
 Glu Pro Val Lys Lys His Pro Leu Val Glu Gly Gly Tyr His Pro His
 180 185 190
 Ile Val Tyr Arg Arg Gln Lys Val Pro Glu Thr Lys Glu Pro Thr Cys
 195 200 205
 Gly Leu Lys Asp Ser Val Asn Ile Ser Gln Lys Gln Glu Leu Trp Arg
 210 215 220
 Glu Lys Trp Glu Arg His Asn Leu Pro Ser Arg Ser Leu Ser Arg Arg
 225 230 235 240
 Ser Ile Ser Lys Glu Arg Trp Val Glu Thr Leu Val Val Ala Asp Thr
 245 250 255
 Lys Met Ile Glu Tyr His Gly Ser Glu Asn Val Glu Ser Tyr Ile Leu
 260 265 270
 Thr Ile Met Asn Met Val Thr Gly Leu Phe His Asn Pro Ser Ile Gly
 275 280 285
 Asn Ala Ile His Ile Val Val Val Arg Leu Ile Leu Leu Glu Glu Glu
 290 295 300
 Glu Gln Gly Leu Lys Ile Val His His Ala Glu Lys Thr Leu Ser Ser
 305 310 315 320
 Phe Cys Lys Trp Gln Lys Ser Ile Asn Pro Lys Ser Asp Leu Asn Pro
 325 330 335

Val His His Asp Val Ala Val Leu Leu Thr Arg Lys Asp Ile Cys Ala
 340 345 350
 Gly Phe Asn Arg Pro Cys Glu Thr Leu Gly Leu Ser His Leu Ser Gly
 355 360 365
 Met Cys Gln Pro His Arg Ser Cys Asn Ile Asn Glu Asp Ser Gly Leu
 370 375 380
 Pro Leu Ala Phe Thr Ile Ala His Glu Leu Gly His Ser Phe Gly Ile
 385 390 395 400
 Gln His Asp Gly Lys Glu Asn Asp Cys Glu Pro Val Gly Arg His Pro
 405 410 415
 Tyr Ile Met Ser Arg Gln Leu Gln Tyr Asp Pro Thr Pro Leu Thr Trp
 420 425 430
 Ser Lys Cys Ser Glu Glu Tyr Ile Thr Arg Phe Leu Asp Arg Gly Trp
 435 440 445
 Gly Phe Cys Leu Asp Asp Ile Pro Lys Lys Lys Gly Leu Lys Ser Lys
 450 455 460
 Val Ile Ala Pro Gly Val Ile Tyr Asp Val His His Gln Cys Gln Leu
 465 470 475 480
 Gln Tyr Gly Pro Asn Ala Thr Phe Cys Gln Glu Val Glu Asn Val Cys
 485 490 495
 Gln Thr Leu Trp Cys Ser Val Lys Gly Phe Cys Arg Ser Lys Leu Asp
 500 505 510
 Ala Ala Ala Asp Gly Thr Gln Cys Gly Glu Lys Lys Trp Cys Met Ala
 515 520 525
 Gly Lys Cys Ile Thr Val Gly Lys Lys Pro Glu Ser Ile Pro Gly Gly
 530 535 540
 Trp Gly Arg Trp Ser Pro Trp Ser His Cys Ser Arg Thr Cys Gly Ala
 545 550 555 560
 Gly Val Gln Ser Ala Glu Arg Leu Cys Asn Asn Pro Glu Pro Lys Phe
 565 570 575
 Gly Gly Lys Tyr Cys Thr Gly Glu Arg Lys Arg Tyr Arg Leu Cys Asn
 580 585 590
 Val His Pro Cys Arg Ser Glu Ala Pro Thr Phe Arg Gln Met Gln Cys
 595 600 605
 Ser Glu Phe Asp Thr Val Pro Tyr Lys Asn Glu Leu Tyr His Trp Phe
 610 615 620
 Pro Ile Phe Asn Pro Ala His Pro Cys Glu Leu Tyr Cys Arg Pro Ile
 625 630 635 640

Asp Gly Gln Phe Ser Glu Lys Met Leu Asp Ala Val Ile Asp Gly Thr
 645 650 655
 Pro Cys Phe Glu Gly Gly Asn Ser Arg Asn Val Cys Ile Asn Gly Ile
 660 665 670
 Cys Lys Met Val Gly Cys Asp Tyr Glu Ile Asp Ser Asn Ala Thr Glu
 675 680 685
 Asp Arg Cys Gly Val Cys Leu Gly Asp Gly Ser Ser Cys Gln Thr Val
 690 695 700
 Arg Lys Met Phe Lys Gln Lys Glu Gly Ser Gly Tyr Val Asp Ile Gly
 705 710 715 720
 Leu Ile Pro Lys Gly Ala Arg Asp Ile Arg Val Met Glu Ile Glu Gly
 725 730 735
 Ala Gly Asn Phe Leu Ala Ile Arg Ser Glu Asp Pro Glu Lys Tyr Tyr
 740 745 750
 Leu Asn Gly Gly Phe Ile Ile Gln Trp Asn Gly Asn Tyr Lys Leu Ala
 755 760 765
 Gly Thr Val Phe Gln Tyr Asp Arg Lys Gly Asp Leu Glu Lys Leu Met
 770 775 780
 Ala Thr Gly Pro Thr Asn Glu Ser Val Trp Ile Gln Leu Leu Phe Gln
 785 790 795 800
 Val Thr Asn Pro Gly Ile Lys Tyr Glu Tyr Thr Ile Gln Lys Asp Gly
 805 810 815
 Leu Asp Asn Asp Val Glu Gln Met Tyr Phe Trp Gln Tyr Gly His Trp
 820 825 830
 Thr Glu Cys Ser Val Thr Cys Gly Thr Gly Ile Arg Arg Gln Thr Ala
 835 840 845
 His Cys Ile Lys Lys Gly Arg Gly Met Val Lys Ala Thr Phe Cys Asp
 850 855 860
 Pro Glu Thr Gln Pro Asn Gly Arg Gln Lys Lys Cys His Glu Lys Ala
 865 870 875 880
 Cys Pro Pro Arg Trp Trp Ala Gly Glu Trp Glu Ala Cys Ser Ala Thr
 885 890 895
 Cys Gly Pro His Gly Glu Lys Lys Arg Thr Val Leu Cys Ile Gln Thr
 900 905 910
 Met Val Ser Asp Glu Gln Ala Leu Pro Pro Thr Asp Cys Gln His Leu
 915 920 925
 Leu Lys Pro Lys Thr Leu Leu Ser Cys Asn Arg Asp Ile Leu Cys Pro
 930 935 940

Ser Asp Trp Thr Val Gly Asn Trp Ser Glu Cys Ser Val Ser Cys Gly
 945 950 955 960
 Gly Gly Val Arg Ile Arg Ser Val Thr Cys Ala Lys Asn His Asp Glu
 965 970 975
 Pro Cys Asp Val Thr Arg Lys Pro Asn Ser Arg Ala Leu Cys Gly Leu
 980 985 990
 Gln Gln Cys Pro Ser Ser Arg Arg Val Leu Lys Pro Asn Lys Gly Thr
 995 1000 1005
 Ile Ser Asn Gly Lys Asn Pro Pro Thr Leu Lys Pro Val Pro Pro Pro
 1010 1015 1020
 Thr Ser Arg Pro Arg Met Leu Thr Thr Pro Thr Gly Pro Glu Ser Met
 1025 1030 1035 1040
 Ser Thr Ser Thr Pro Ala Ile Ser Ser Pro Ser Pro Thr Thr Ala Ser
 1045 1050 1055
 Lys Glu Gly Asp Leu Gly Gly Lys Gln Trp Gln Asp Ser Ser Thr Gln
 1060 1065 1070
 Pro Glu Leu Ser Ser Arg Tyr Leu Ile Ser Thr Gly Ser Thr Ser Gln
 1075 1080 1085
 Pro Ile Leu Thr Ser Gln Ser Leu Ser Ile Gln Pro Ser Glu Glu Asn
 1090 1095 1100
 Val Ser Ser Ser Asp Thr Gly Pro Thr Ser Glu Gly Gly Leu Val Ala
 1105 1110 1115 1120
 Thr Thr Thr Ser Gly Ser Gly Leu Ser Ser Ser Arg Asn Pro Ile Thr
 1125 1130 1135
 Trp Pro Val Thr Pro Phe Tyr Asn Thr Leu Thr Lys Gly Pro Glu Met
 1140 1145 1150
 Glu Ile His Ser Gly Ser Gly Glu Glu Arg Glu Gln Pro Glu Asp Lys
 1155 1160 1165
 Asp Glu Ser Asn Pro Val Ile Trp Thr Lys Ile Arg Val Pro Gly Asn
 1170 1175 1180
 Asp Ala Pro Val Glu Ser Thr Glu Met Pro Leu Ala Pro Pro Leu Thr
 1185 1190 1195 1200
 Pro Asp Leu Ser Arg Glu Ser Trp Trp Pro Pro Phe Ser Thr Val Met
 1205 1210 1215
 Glu Gly Leu Leu Pro Ser Gln Arg Pro Thr Thr Ser Glu Thr Gly Thr
 1220 1225 1230
 Pro Arg Val Glu Gly Met Val Thr Glu Lys Pro Ala Asn Thr Leu Leu
 1235 1240 1245

Pro Leu Gly Gly Asp His Gln Pro Glu Pro Ser Gly Lys Thr Ala Asn
 1250 1255 1260

Arg Asn His Leu Lys Leu Pro Asn Asn Met Asn Gln Thr Lys Ser Ser
 1265 1270 1275 1280

Glu Pro Val Leu Thr Glu Glu Asp Ala Thr Ser Leu Ile Thr Glu Gly
 1285 1290 1295

Phe Leu Leu Asn Ala Ser Asn Tyr Lys Gln Leu Thr Asn Gly His Gly
 1300 1305 1310

Ser Ala His Trp Ile Val Gly Asn Trp Ser Glu Cys Ser Thr Thr Cys
 1315 1320 1325

Gly Leu Gly Ala Tyr Trp Lys Arg Val Glu Cys Thr Thr Gln Met Asp
 1330 1335 1340

Ser Asp Cys Ala Ala Ile Gln Arg Pro Asp Pro Ala Lys Arg Cys His
 1345 1350 1355 1360

Leu Arg Pro Cys Ala Gly Trp Lys Val Gly Asn Trp Ser Lys Cys Ser
 1365 1370 1375

Arg Asn Cys Ser Gly Gly Phe Lys Ile Arg Glu Ile Gln Cys Val Asp
 1380 1385 1390

Ser Arg Asp His Arg Asn Leu Arg Pro Phe His Cys Gln Phe Leu Ala
 1395 1400 1405

Gly Ile Pro Pro Pro Leu Ser Met Ser Cys Asn Pro Glu Pro Cys Glu
 1410 1415 1420

Ala Trp Gln Val Glu Pro Trp Ser Gln Cys Ser Arg Ser Cys Gly Gly
 1425 1430 1435 1440

Gly Val Gln Glu Arg Gly Val Phe Cys Pro Gly Gly Leu Cys Asp Trp
 1445 1450 1455

Thr Lys Arg Pro Thr Ser Thr Met Ser Cys Asn Glu His Leu Cys Cys
 1460 1465 1470

His Trp Ala Thr Gly Asn Trp Asp Leu Cys Ser Thr Ser Cys Gly Gly
 1475 1480 1485

Gly Phe Gln Lys Arg Ile Val Gln Cys Val Pro Ser Glu Gly Asn Lys
 1490 1495 1500

Thr Glu Asp Gln Asp Gln Cys Leu Cys Asp His Lys Pro Arg Pro Pro
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Glu Phe Lys Lys Cys Asn Gln Gln Ala Cys Lys Lys Ser Ala Asp Leu
 1525 1530 1535

Leu Cys Thr Lys Asp Lys Leu Ser Ala Ser Phe Cys Gln Thr Leu Lys
 1540 1545 1550

Ala Met Lys Lys Cys Ser Val Pro Thr Val Arg Ala Glu Cys Cys Phe
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Ser Cys Pro Gln Thr His Ile Thr His Thr Gln Arg Gln Arg Arg Gln
 1570 1575 1580

Arg Leu Leu Gln Lys Ser Lys Glu Leu
 1585 1590

<210> 31
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 <212> PRT
 <213> Homo sapiens

<400> 31
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Pro Pro Pro Arg Arg Gln Arg Arg Gly Thr Gly Ala Thr Ala Glu Ser
 35 40 45

Arg Leu Phe Tyr Lys Val Ala Ser Pro Ser Thr His Phe Leu Leu Asn
 50 55 60

Leu Thr Arg Ser Ser Arg Leu Leu Ala Gly His Val Ser Val Glu Tyr
 65 70 75 80

Trp Thr Arg Glu Gly Leu Ala Trp Gln Arg Ala Ala Arg Pro His Cys
 85 90 95

Leu Tyr Ala Gly His Leu Gln Gly Gln Ala Ser Ser Ser His Val Ala
 100 105 110

Ile Ser Thr Cys Gly Gly Leu His Gly Leu Ile Val Ala Asp Glu Glu
 115 120 125

Glu Tyr Leu Ile Glu Pro Leu His Gly Gly Pro Lys Gly Ser Arg Ser
 130 135 140

Pro Glu Glu Ser Gly Pro His Val Val Tyr Lys Arg Ser Ser Leu Arg
 145 150 155 160

His Pro His Leu Asp Thr Ala Cys Gly Val Arg Asp Glu Lys Pro Trp
 165 170 175

Lys Gly Arg Pro Trp Trp Leu Arg Thr Leu Lys Pro Pro Pro Ala Arg
 180 185 190

Pro Leu Gly Asn Glu Thr Glu Arg Gly Gln Pro Gly Leu Lys Arg Ser
 195 200 205

Val Ser Arg Glu Arg Tyr Val Glu Thr Leu Val Val Ala Asp Lys Met

210	215	220
Met Val Ala Tyr His Gly Arg Arg Asp Val Glu Gln Tyr Val Leu Ala 225 230 235 240		
Ile Met Asn Ile Val Ala Lys Leu Phe Gln Asp Ser Ser Leu Gly Ser 245 250 255		
Thr Val Asn Ile Leu Val Thr Arg Leu Ile Leu Leu Thr Glu Asp Gln 260 265 270		
Pro Thr Leu Glu Ile Thr His His Ala Gly Lys Ser Leu Asp Ser Phe 275 280 285		
Cys Lys Trp Gln Lys Ser Ile Val Asn His Ser Gly His Gly Asn Ala 290 295 300		
Ile Pro Glu Asn Gly Val Ala Asn His Asp Thr Ala Val Leu Ile Thr 305 310 315 320		
Arg Tyr Asp Ile Cys Ile Tyr Lys Asn Lys Pro Cys Gly Thr Leu Gly 325 330 335		
Leu Ala Pro Val Gly Gly Met Cys Glu Arg Glu Arg Ser Cys Ser Val 340 345 350		
Asn Glu Asp Ile Gly Leu Pro Gln Ala Phe Thr Ile Ala His Glu Ile 355 360 365		
Gly His Thr Phe Gly Met Asn His Asp Gly Val Gly Asn Ser Cys Gly 370 375 380		
Ala Arg Gly Gln Asp Pro Ala Lys Leu Met Ala Ala His Ile Thr Met 385 390 395 400		
Lys Thr Asn Pro Phe Val Trp Ser Ser Cys Asn Arg Asp Tyr Ile Thr 405 410 415		
Ser Phe Leu Asp Ser Gly Leu Gly Leu Cys Leu Asn Asn Arg Pro Pro 420 425 430		
Arg Gln Asp Phe Val Tyr Pro Thr Val Ala Pro Gly Gln Ala Tyr Asp 435 440 445		
Ala Asp Glu Gln Cys Arg Phe Gln His Gly Val Lys Ser Arg Gln Cys 450 455 460		
Lys Tyr Gly Glu Val Cys Ser Glu Leu Trp Cys Leu Ser Lys Ser Asn 465 470 475 480		
Arg Cys Ile Thr Asn Ser Ile Pro Ala Ala Glu Gly Thr Leu Cys Gln 485 490 495		
Thr His Thr Ile Asp Lys Gly Trp Cys Tyr Lys Arg Val Cys Val Pro 500 505 510		
Phe Gly Ser Arg Pro Glu Gly Val Asp Gly Ala Trp Gly Pro Trp Thr		

515	520	525
Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val Ser Ser Ser		
530	535	540
Ser Arg His Cys Asp Ser Pro Arg Pro Thr Ile Gly Gly Lys Tyr Cys		
545	550	555
Leu Gly Glu Arg Arg Arg His Arg Ser Cys Asn Thr Asp Asp Cys Pro		
	565	570
Pro Gly Ser Gln Asp Phe Arg Glu Val Gln Cys Ser Glu Phe Asp Ser		
	580	585
Ile Pro Phe Arg Gly Lys Phe Tyr Lys Trp Lys Thr Tyr Arg Gly Gly		
	595	600
Gly Val Lys Ala Cys Ser Leu Thr Ser Leu Ala Glu Gly Phe Asn Phe		
	610	615
Tyr Thr Glu Arg Ala Ala Ala Val Val Asp Gly Thr Pro Cys Arg Pro		
	625	630
Asp Thr Val Asp Ile Cys Val Ser Gly Glu Cys Lys His Val Gly Cys		
	645	650
Asp Arg Val Leu Gly Ser Asp Leu Arg Glu Asp Lys Cys Arg Val Cys		
	660	665
Gly Gly Asp Gly Ser Ala Cys Glu Thr Ile Glu Gly Val Phe Ser Pro		
	675	680
Ala Ser Pro Gly Ala Gly Tyr Glu Asp Val Val Trp Ile Pro Lys Gly		
	690	695
Ser Val His Ile Phe Ile Gln Asp Leu Asn Leu Ser Leu Ser His Leu		
	705	710
Ala Leu Lys Gly Asp Gln Glu Ser Leu Leu Leu Glu Gly Leu Pro Gly		
	725	730
Thr Pro Gln Pro His Arg Leu Pro Leu Ala Gly Thr Thr Phe Gln Leu		
	740	745
Arg Gln Gly Pro Asp Gln Val Gln Ser Leu Glu Ala Leu Gly Pro Ile		
	755	760
Asn Ala Ser Leu Ile Val Met Val Leu Ala Arg Thr Glu Leu Pro Ala		
	770	775
Leu Arg Tyr Arg Phe Asn Ala Pro Ile Ala Arg Asp Ser Leu Pro Pro		
	785	790
Tyr Ser Trp His Tyr Ala Pro Trp Thr Lys Cys Ser Ala Gln Cys Ala		
	805	810
Gly Gly Ser Gln Val Gln Ala Val Glu Cys Arg Asn Gln Leu Asp Ser		
		815

820					825					830						
Ser	Ala	Val	Ala	Pro	His	Tyr	Cys	Ser	Ala	His	Ser	Lys	Leu	Pro	Lys	
835					840					845						
Arg	Gln	Arg	Ala	Cys	Asn	Thr	Glu	Pro	Cys	Pro	Pro	Asp	Trp	Val	Val	
850					855					860						
Gly	Asn	Trp	Ser	Leu	Cys	Ser	Arg	Ser	Cys	Asp	Ala	Gly	Val	Arg	Ser	
865					870					875					880	
Arg	Ser	Val	Val	Cys	Gln	Arg	Arg	Val	Ser	Ala	Ala	Glu	Glu	Lys	Ala	
885					890					895						
Leu	Asp	Asp	Ser	Ala	Cys	Pro	Gln	Pro	Arg	Pro	Pro	Val	Leu	Glu	Ala	
900					905					910						
Cys	His	Gly	Pro	Thr	Cys	Pro	Pro	Glu	Trp	Ala	Ala	Leu	Asp	Trp	Ser	
915					920					925						
Glu	Cys	Thr	Pro	Ser	Cys	Gly	Pro	Gly	Leu	Arg	His	Arg	Val	Val	Leu	
930					935					940						
Cys	Lys	Ser	Ala	Asp	His	Arg	Ala	Thr	Leu	Pro	Pro	Ala	His	Cys	Ser	
945					950					955					960	
Pro	Ala	Ala	Lys	Pro	Pro	Ala	Thr	Met	Arg	Cys	Asn	Leu	Arg	Arg	Cys	
965					970					975						
Pro	Pro	Ala	Arg	Trp	Val	Ala	Gly	Glu	Trp	Gly	Glu	Cys	Ser	Ala	Gln	
980					985					990						
Cys	Gly	Val	Gly	Gln	Arg	Gln	Arg	Ser	Val	Arg	Cys	Thr	Ser	His	Thr	
995					1000					1005						
Gly	Gln	Ala	Ser	His	Glu	Cys	Thr	Glu	Ala	Leu	Arg	Pro	Pro	Thr	Thr	
1010					1015					1020						
Gln	Gln	Cys	Glu	Ala	Lys	Cys	Asp	Ser	Pro	Thr	Pro	Gly	Asp	Gly	Pro	
1025					1030					1035					1040	
Glu	Glu	Cys	Lys	Asp	Val	Asn	Lys	Val	Ala	Tyr	Cys	Pro	Leu	Val	Leu	
1045					1050					1055						
Lys	Phe	Gln	Phe	Cys	Ser	Arg	Ala	Tyr	Phe	Arg	Gln	Met	Cys	Cys	Lys	
1060					1065					1070						
Thr	Cys	Gln	Gly	His												
1075																

<210> 32

<211> 997

<212> PRT

<213> Homo sapiens

<400> 32

Met Pro Gly Gly Pro Ser Pro Arg Ser Pro Ala Pro Leu Leu Arg Pro
 1 5 10 15
 Leu Leu Leu Leu Leu Cys Ala Leu Ala Pro Gly Ala Pro Gly Pro Ala
 20 25 30
 Pro Gly Arg Ala Thr Glu Gly Arg Ala Ala Leu Asp Ile Val His Pro
 35 40 45
 Val Arg Val Asp Ala Gly Gly Ser Phe Leu Ser Tyr Glu Leu Trp Pro
 50 55 60
 Arg Ala Leu Arg Lys Arg Asp Val Ser Val Arg Arg Asp Ala Pro Ala
 65 70 75 80
 Phe Tyr Glu Leu Gln Tyr Arg Gly Arg Glu Leu Arg Phe Asn Leu Thr
 85 90 95
 Ala Asn Gln His Leu Leu Ala Pro Gly Phe Val Ser Glu Thr Arg Arg
 100 105 110
 Arg Gly Gly Leu Gly Arg Ala His Ile Arg Ala His Thr Pro Ala Cys
 115 120 125
 His Leu Leu Gly Glu Val Gln Asp Pro Glu Leu Glu Gly Gly Leu Ala
 130 135 140
 Ala Ile Ser Ala Cys Asp Gly Leu Lys Gly Val Phe Gln Leu Ser Asn
 145 150 155 160
 Glu Asp Tyr Phe Ile Glu Pro Leu Asp Ser Ala Pro Ala Arg Pro Gly
 165 170 175
 His Ala Gln Pro His Val Val Tyr Lys Arg Gln Ala Pro Glu Arg Leu
 180 185 190
 Ala Gln Arg Gly Asp Ser Ser Ala Pro Ser Thr Cys Gly Val Gln Val
 195 200 205
 Tyr Pro Glu Leu Glu Ser Arg Arg Glu Arg Trp Glu Gln Arg Gln Gln
 210 215 220
 Trp Arg Arg Pro Arg Leu Arg Arg Leu His Gln Arg Ser Val Ser Lys
 225 230 235 240
 Glu Lys Trp Val Glu Thr Leu Val Val Ala Asp Ala Lys Met Val Glu
 245 250 255
 Tyr His Gly Gln Pro Gln Val Glu Ser Tyr Val Leu Thr Ile Met Asn
 260 265 270
 Met Val Ala Gly Leu Phe His Asp Pro Ser Ile Gly Asn Pro Ile His
 275 280 285
 Ile Thr Ile Val Arg Leu Val Leu Leu Glu Asp Glu Glu Glu Asp Leu
 290 295 300

Lys	Ile	Thr	His	His	Ala	Asp	Asn	Thr	Leu	Lys	Ser	Phe	Cys	Lys	Trp	305	310	315	320
Gln	Lys	Ser	Ile	Asn	Met	Lys	Gly	Asp	Ala	His	Pro	Leu	His	His	Asp	325	330	335	
Thr	Ala	Ile	Leu	Leu	Thr	Arg	Lys	Asp	Leu	Cys	Ala	Ala	Met	Asn	Arg	340	345	350	
Pro	Cys	Glu	Thr	Leu	Gly	Leu	Ser	His	Val	Ala	Gly	Met	Cys	Gln	Pro	355	360	365	
His	Arg	Ser	Cys	Ser	Ile	Asn	Glu	Asp	Thr	Gly	Leu	Pro	Leu	Ala	Phe	370	375	380	
Thr	Val	Ala	His	Glu	Leu	Gly	His	Ser	Phe	Gly	Ile	Gln	His	Asp	Gly	385	390	395	400
Ser	Gly	Asn	Asp	Cys	Glu	Pro	Val	Gly	Lys	Arg	Pro	Phe	Ile	Met	Ser	405	410	415	
Pro	Gln	Leu	Leu	Tyr	Asp	Ala	Ala	Pro	Leu	Thr	Trp	Ser	Arg	Cys	Ser	420	425	430	
Arg	Gln	Tyr	Ile	Thr	Arg	Phe	Leu	Asp	Arg	Gly	Trp	Gly	Leu	Cys	Leu	435	440	445	
Asp	Asp	Pro	Pro	Ala	Lys	Asp	Ile	Ile	Asp	Phe	Pro	Ser	Val	Pro	Pro	450	455	460	
Gly	Val	Leu	Tyr	Asp	Val	Ser	His	Gln	Cys	Arg	Leu	Gln	Tyr	Gly	Ala	465	470	475	480
Tyr	Ser	Ala	Phe	Cys	Glu	Asp	Met	Asp	Asn	Val	Cys	His	Thr	Leu	Trp	485	490	495	
Cys	Ser	Val	Gly	Thr	Thr	Cys	His	Ser	Lys	Leu	Asp	Ala	Ala	Val	Asp	500	505	510	
Gly	Thr	Arg	Cys	Gly	Glu	Asn	Lys	Trp	Cys	Leu	Ser	Gly	Glu	Cys	Val	515	520	525	
Pro	Val	Gly	Phe	Arg	Pro	Glu	Ala	Val	Asp	Gly	Gly	Trp	Ser	Gly	Trp	530	535	540	
Ser	Ala	Trp	Ser	Ile	Cys	Ser	Arg	Ser	Cys	Gly	Met	Gly	Val	Gln	Ser	545	550	555	560
Ala	Glu	Arg	Gln	Cys	Thr	Gln	Pro	Thr	Pro	Lys	Tyr	Lys	Gly	Arg	Tyr	565	570	575	
Cys	Val	Gly	Glu	Arg	Lys	Arg	Phe	Arg	Leu	Cys	Asn	Leu	Gln	Ala	Cys	580	585	590	
Pro	Ala	Gly	Arg	Pro	Ser	Phe	Arg	His	Val	Gln	Cys	Ser	His	Phe	Asp	595	600	605	

Ala Met Leu Tyr Lys Gly Gln Leu His Thr Trp Val Pro Val Val Asn
 610 615 620
 Asp Val Asn Pro Cys Glu Leu His Cys Arg Pro Ala Asn Glu Tyr Phe
 625 630 635 640
 Ala Lys Lys Leu Arg Asp Ala Val Val Asp Gly Thr Pro Cys Tyr Gln
 645 650 655
 Val Arg Ala Ser Arg Asp Leu Cys Ile Asn Gly Ile Cys Lys Asn Val
 660 665 670
 Gly Cys Asp Phe Glu Ile Asp Ser Gly Ala Met Glu Asp Arg Cys Gly
 675 680 685
 Val Cys His Gly Asn Gly Ser Thr Cys His Thr Val Ser Gly Thr Phe
 690 695 700
 Glu Glu Ala Glu Gly Leu Gly Tyr Val Asp Val Gly Leu Ile Pro Ala
 705 710 715 720
 Gly Ala Arg Glu Ile Arg Ile Gln Glu Val Ala Glu Ala Ala Asn Phe
 725 730 735
 Leu Ala Leu Arg Ser Glu Asp Pro Glu Lys Tyr Phe Leu Asn Gly Gly
 740 745 750
 Trp Thr Ile Gln Trp Asn Gly Asp Tyr Gln Val Ala Gly Thr Thr Phe
 755 760 765
 Thr Tyr Ala Arg Arg Gly Asn Trp Glu Asn Leu Thr Ser Pro Gly Pro
 770 775 780
 Thr Lys Glu Pro Val Trp Ile Gln Val Pro Ala Ser Arg Gly Pro Gly
 785 790 795 800
 Gly Gly Ser Arg Gly Gly Val Pro Arg Pro Ser Thr Leu His Gly Arg
 805 810 815
 Ser Arg Pro Gly Gly Val Ser Pro Gly Ser Val Thr Glu Pro Gly Ser
 820 825 830
 Glu Pro Gly Pro Pro Ala Ala Ala Ser Thr Ser Val Ser Pro Ser Leu
 835 840 845
 Lys Trp Pro Asn Leu Val Ala Ala Val His Arg Gly Gly Trp Gly Gln
 850 855 860
 Ala Pro Leu Gly Leu Gly Gly Trp Arg Arg His Leu Val Leu Met Gly
 865 870 875 880
 Pro Arg Leu Pro Thr Gln Leu Leu Phe Gln Glu Ser Asn Pro Gly Val
 885 890 895
 His Tyr Glu Tyr Thr Ile His Arg Glu Ala Gly Gly His Asp Glu Val
 900 905 910

Pro Pro Pro Val Phe Ser Trp His Tyr Gly Pro Trp Thr Lys Cys Thr
 915 920 925
 Val Thr Cys Gly Arg Gly Glu Lys Trp Gly Arg His Ser Pro Thr Cys
 930 935 940
 Arg Gly Leu Val Ser Gly Gln Gly His Trp Leu Gln Leu Pro Ala His
 945 950 955 960
 Cys Trp Ala Thr Thr Gly Leu Glu Val Cys Phe Ser Glu Pro Gln Phe
 965 970 975
 Ser Ile Cys Glu Met Arg Leu Ala Ile Ala Leu Cys Pro Arg Pro Ala
 980 985 990
 Gly Arg Val His Gly
 995

<210> 33
 <211> 854
 <212> PRT
 <213> Homo sapiens

<400> 33
 Met Met Val Ala Tyr His Gly Arg Arg Asp Val Glu Gln Tyr Val Leu
 1 5 10 15
 Ala Ile Met Asn Ile Val Ala Lys Leu Phe Gln Asp Ser Ser Leu Gly
 20 25 30
 Ser Thr Val Asn Ile Leu Val Thr Arg Leu Ile Leu Leu Thr Glu Asp
 35 40 45
 Gln Pro Thr Leu Glu Ile Thr His His Ala Gly Lys Ser Leu Asp Ser
 50 55 60
 Phe Cys Lys Trp Gln Lys Ser Ile Val Asn His Ser Gly His Gly Asn
 65 70 75 80
 Ala Ile Pro Glu Asn Gly Val Ala Asn His Asp Thr Ala Val Leu Ile
 85 90 95
 Thr Arg Tyr Asp Ile Cys Ile Tyr Lys Asn Lys Pro Cys Gly Thr Leu
 100 105 110
 Gly Leu Ala Pro Val Gly Gly Met Cys Glu Arg Glu Arg Ser Cys Ser
 115 120 125
 Val Asn Glu Asp Ile Gly Leu Ala Thr Ala Phe Thr Ile Ala His Glu
 130 135 140
 Ile Gly His Thr Phe Gly Met Asn His Asp Gly Val Gly Asn Ser Cys
 145 150 155 160
 Gly Ala Arg Gly Gln Asp Pro Ala Lys Leu Met Ala Ala His Ile Thr
 165 170 175

Met Lys Thr Asn Pro Phe Val Trp Ser Ser Cys Ser Arg Asp Tyr Ile
 180 185 190
 Thr Ser Phe Leu Asp Ser Gly Leu Gly Leu Cys Leu Asn Asn Arg Pro
 195 200 205
 Pro Arg Gln Asp Phe Val Tyr Pro Thr Val Ala Pro Gly Gln Ala Tyr
 210 215 220
 Asp Ala Asp Glu Gln Cys Arg Phe Gln His Gly Val Lys Ser Arg Gln
 225 230 235 240
 Cys Lys Tyr Gly Glu Val Cys Ser Glu Leu Trp Cys Leu Ser Lys Ser
 245 250 255
 Asn Arg Cys Ile Thr Asn Ser Ile Pro Ala Ala Glu Gly Thr Leu Cys
 260 265 270
 Gln Thr His Thr Ile Asp Lys Gly Trp Cys Tyr Lys Arg Val Cys Val
 275 280 285
 Pro Phe Gly Ser Arg Pro Glu Gly Val Asp Gly Ala Trp Gly Pro Trp
 290 295 300
 Thr Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val Ser Ser
 305 310 315 320
 Ser Ser Arg His Cys Asp Ser Pro Arg Pro Thr Ile Gly Gly Lys Tyr
 325 330 335
 Cys Leu Gly Glu Arg Arg Arg His Arg Ser Cys Asn Thr Asp Asp Cys
 340 345 350
 Pro Pro Gly Ser Gln Asp Phe Arg Glu Val Gln Cys Ser Glu Phe Asp
 355 360 365
 Ser Ile Pro Phe Arg Gly Lys Phe Tyr Lys Trp Lys Thr Tyr Arg Gly
 370 375 380
 Gly Gly Val Lys Ala Cys Ser Leu Thr Cys Leu Ala Glu Gly Phe Asn
 385 390 395 400
 Phe Tyr Thr Glu Arg Ala Ala Ala Val Val Asp Gly Thr Pro Cys Arg
 405 410 415
 Pro Asp Thr Val Asp Ile Cys Val Ser Gly Glu Cys Lys His Val Gly
 420 425 430
 Cys Asp Arg Val Leu Gly Ser Asp Leu Arg Glu Asp Lys Cys Arg Val
 435 440 445
 Cys Gly Gly Asp Gly Ser Ala Cys Glu Thr Ile Glu Gly Val Phe Ser
 450 455 460
 Pro Ala Ser Pro Gly Ala Gly Tyr Glu Asp Val Val Trp Ile Pro Lys
 465 470 475 480

Gly Ser Val His Ile Phe Ile Gln Asp Leu Asn Leu Ser Leu Ser His
 485 490 495
 Leu Ala Leu Lys Gly Asp Gln Glu Ser Leu Leu Leu Glu Gly Leu Pro
 500 505 510
 Gly Thr Pro Gln Pro His Arg Leu Pro Leu Ala Gly Thr Thr Phe Gln
 515 520 525
 Leu Arg Gln Gly Pro Asp Gln Val Gln Ser Leu Glu Ala Leu Gly Pro
 530 535 540
 Ile Asn Ala Ser Leu Ile Val Met Val Leu Ala Arg Thr Glu Leu Pro
 545 550 555 560
 Ala Leu Arg Tyr Arg Phe Asn Ala Pro Ile Ala Arg Asp Ser Leu Pro
 565 570 575
 Pro Tyr Ser Trp His Tyr Ala Pro Trp Thr Lys Cys Ser Ala Gln Cys
 580 585 590
 Ala Gly Gly Ser Gln Val Gln Ala Val Glu Cys Arg Asn Gln Leu Asp
 595 600 605
 Ser Ser Ala Val Ala Pro His Tyr Cys Ser Ala His Ser Lys Leu Pro
 610 615 620
 Lys Arg Gln Arg Ala Cys Asn Thr Glu Pro Cys Pro Pro Asp Trp Val
 625 630 635 640
 Val Gly Asn Trp Ser Leu Cys Ser Arg Ser Cys Asp Ala Gly Val Arg
 645 650 655
 Ser Arg Ser Val Val Cys Gln Arg Arg Val Ser Ala Ala Glu Glu Lys
 660 665 670
 Ala Leu Asp Asp Ser Ala Cys Pro Gln Pro Arg Pro Pro Val Leu Glu
 675 680 685
 Ala Cys His Gly Pro Thr Cys Pro Pro Glu Trp Ala Ala Leu Asp Trp
 690 695 700
 Ser Glu Cys Thr Pro Ser Cys Gly Pro Gly Leu Arg His Arg Val Val
 705 710 715 720
 Leu Cys Lys Ser Ala Asp His Arg Ala Thr Leu Pro Pro Ala His Cys
 725 730 735
 Ser Pro Ala Ala Lys Pro Pro Ala Thr Met Arg Cys Asn Leu Arg Arg
 740 745 750
 Cys Pro Pro Ala Arg Trp Val Ala Gly Glu Trp Gly Glu Cys Ser Ala
 755 760 765
 Gln Cys Gly Val Gly Gln Arg Gln Arg Ser Val Arg Cys Thr Ser His
 770 775 780

Thr Gly Gln Ala Ser His Glu Cys Thr Glu Ala Leu Arg Pro Pro Thr
785 790 795 800

Thr Gln Gln Cys Glu Ala Lys Cys Asp Ser Pro Thr Pro Gly Asp Gly
805 810 815

Pro Glu Glu Cys Lys Asp Val Asn Lys Val Ala Tyr Cys Pro Leu Val
820 825 830

Leu Lys Phe Gln Phe Cys Ser Arg Ala Tyr Phe Arg Gln Met Cys Cys
835 840 845

Lys Thr Cys His Gly His
850

<210> 34

<211> 860

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (450)

<223> Wherein Xaa is any amino acid.

<400> 34

Met Glu Ile Leu Trp Lys Thr Leu Thr Trp Ile Leu Ser Leu Ile Met
1 5 10 15

Ala Ser Ser Glu Phe His Ser Asp His Arg Leu Ser Tyr Ser Ser Gln
20 25 30

Glu Glu Phe Leu Thr Tyr Leu Glu His Tyr Gln Leu Thr Ile Pro Ile
35 40 45

Arg Val Asp Gln Asn Gly Ala Phe Leu Ser Phe Thr Val Lys Asn Asp
50 55 60

Lys His Ser Arg Arg Arg Arg Ser Met Asp Pro Ile Asp Pro Gln Gln
65 70 75 80

Ala Val Ser Lys Leu Phe Phe Lys Leu Ser Ala Tyr Gly Lys His Phe
85 90 95

His Leu Asn Leu Thr Leu Asn Thr Asp Phe Val Ser Lys His Phe Thr
100 105 110

Val Glu Tyr Trp Gly Lys Asp Gly Pro Gln Trp Lys His Asp Phe Leu
115 120 125

Asp Asn Cys His Tyr Thr Gly Tyr Leu Gln Asp Gln Arg Ser Thr Thr
130 135 140

Lys Val Ala Leu Ser Asn Cys Val Gly Leu His Gly Val Ile Ala Thr
145 150 155 160

Glu Asp Glu Glu Tyr Phe Ile Glu Pro Leu Lys Asn Thr Thr Glu Asp
 165 170 175
 Ser Lys His Phe Ser Tyr Glu Asn Gly His Pro His Val Ile Tyr Lys
 180 185 190
 Lys Ser Ala Leu Gln Gln Arg His Leu Tyr Asp His Ser His Cys Gly
 195 200 205
 Val Ser Asp Phe Thr Arg Ser Gly Lys Pro Trp Trp Leu Asn Asp Thr
 210 215 220
 Ser Thr Val Ser Tyr Ser Leu Pro Ile Asn Asn Thr His Ile His His
 225 230 235 240
 Arg Gln Lys Arg Ser Val Ser Ile Glu Arg Phe Val Glu Thr Leu Val
 245 250 255
 Val Ala Asp Lys Met Met Val Gly Tyr His Gly Arg Lys Asp Ile Glu
 260 265 270
 His Tyr Ile Leu Ser Val Met Asn Ile Val Ala Lys Leu Tyr Arg Asp
 275 280 285
 Ser Ser Leu Gly Asn Val Val Asn Ile Ile Val Ala Arg Leu Ile Val
 290 295 300
 Leu Thr Glu Asp Gln Pro Asn Leu Glu Ile Asn His His Ala Asp Lys
 305 310 315 320
 Ser Leu Asp Ser Phe Cys Lys Trp Gln Lys Ser Ile Leu Ser His Gln
 325 330 335
 Ser Asp Gly Asn Thr Ile Pro Glu Asn Gly Ile Ala His His Asp Asn
 340 345 350
 Ala Val Leu Ile Thr Arg Tyr Asp Ile Cys Thr Tyr Lys Asn Lys Pro
 355 360 365
 Cys Gly Thr Leu Gly Leu Ala Ser Val Ala Gly Met Cys Glu Pro Glu
 370 375 380
 Arg Ser Cys Ser Ile Asn Glu Asp Ile Gly Leu Gly Ser Ala Phe Thr
 385 390 395 400
 Ile Ala His Glu Ile Val His Asn Phe Gly Met Asn His Asp Gly Ile
 405 410 415
 Gly Asn Ser Cys Gly Arg Lys Val Met Lys Gln Gln Asn Tyr Gly Ser
 420 425 430
 Ser His Tyr Cys Glu Tyr Gln Ser Phe Phe Leu Val Cys Leu Gln Ser
 435 440 445
 Arg Xaa His His Gln Leu Phe Arg Glu Val Cys Arg Glu Leu Trp Cys
 450 455 460

Leu Ser Lys Ser Asn Arg Cys Val Thr Asn Ser Ile Pro Ala Ala Glu
 465 470 475 480
 Gly Thr Leu Cys Gln Thr Gly Asn Ile Glu Lys Gly Trp Cys Tyr Gln
 485 490 495
 Gly Asp Cys Val Pro Phe Gly Thr Trp Pro Gln Ser Ile Asp Gly Gly
 500 505 510
 Trp Gly Pro Trp Ser Leu Trp Gly Glu Cys Ser Arg Thr Cys Gly Gly
 515 520 525
 Gly Val Ser Ser Ser Leu Arg His Cys Asp Ser Pro Ala Pro Ser Gly
 530 535 540
 Gly Gly Lys Tyr Cys Leu Gly Glu Arg Lys Arg Tyr Arg Ser Cys Asn
 545 550 555 560
 Thr Asp Pro Cys Pro Leu Gly Ser Arg Asp Phe Arg Glu Lys Gln Cys
 565 570 575
 Ala Asp Phe Asp Asn Met Pro Phe Arg Gly Lys Tyr Tyr Asn Trp Lys
 580 585 590
 Pro Tyr Thr Gly Gly Gly Val Lys Pro Cys Ala Leu Asn Cys Leu Ala
 595 600 605
 Glu Gly Tyr Asn Phe Tyr Thr Glu Arg Ala Pro Ala Val Ile Asp Gly
 610 615 620
 Thr Gln Cys Asn Ala Asp Ser Leu Asp Ile Cys Ile Asn Gly Glu Cys
 625 630 635 640
 Lys His Val Gly Cys Asp Asn Ile Leu Gly Ser Asp Ala Arg Glu Asp
 645 650 655
 Arg Cys Arg Val Cys Gly Gly Gly Gly Ser Thr Cys Asp Ala Ile Glu
 660 665 670
 Gly Phe Phe Asn Asp Ser Leu Pro Arg Gly Gly Tyr Met Glu Val Val
 675 680 685
 Gln Ile Pro Arg Gly Ser Val His Ile Glu Val Arg Glu Val Ala Met
 690 695 700
 Ser Lys Asn Tyr Ile Ala Leu Lys Ser Glu Gly Asp Asp Tyr Tyr Ile
 705 710 715 720
 Asn Gly Ala Trp Thr Ile Asp Trp Pro Arg Lys Phe Asp Val Ala Gly
 725 730 735
 Thr Ala Phe His Tyr Lys Arg Pro Thr Asp Glu Pro Glu Ser Leu Glu
 740 745 750
 Ala Leu Gly Pro Thr Ser Glu Asn Leu Ile Val Met Val Leu Leu Gln
 755 760 765

Glu Gln Asn Leu Gly Ile Arg Tyr Lys Phe Asn Val Pro Ile Thr Arg
 770 775 780

Thr Gly Ser Gly Asp Asn Glu Val Gly Phe Thr Trp Asn His Gln Pro
 785 790 795 800

Trp Ser Glu Cys Ser Ala Thr Cys Ala Gly Gly Lys Met Pro Thr Arg
 805 810 815

Gln Pro Thr Gln Arg Ala Arg Trp Arg Thr Lys His Ile Leu Ser Tyr
 820 825 830

Ala Leu Cys Leu Leu Lys Lys Leu Ile Gly Asn Ile Ser Cys Arg Phe
 835 840 845

Ala Ser Ser Cys Asn Leu Ala Lys Glu Thr Leu Leu
 850 855 860

<210> 35
 <211> 936
 <212> PRT
 <213> Homo sapiens

<400> 35
 Arg Leu Leu Ile Tyr Ala Val Leu Pro Thr Gly Asp Val Ile Gly Asp
 1 5 10 15

Ser Ala Lys Tyr Asp Val Glu Asn Cys Leu Ala Asn Lys Val Asp Leu
 20 25 30

Ser Phe Ser Pro Ser Gln Ser Leu Pro Ala Ser His Ala His Leu Arg
 35 40 45

Val Thr Ala Ala Pro Gln Ser Val Cys Ala Leu Arg Ala Val Asp Gln
 50 55 60

Ser Val Leu Leu Met Lys Pro Asp Ala Glu Leu Ser Ala Ser Ser Val
 65 70 75 80

Tyr Asn Leu Leu Pro Glu Lys Asp Leu Thr Gly Phe Pro Gly Pro Leu
 85 90 95

Asn Asp Gln Asp Asn Glu Asp Cys Ile Asn Arg His Asn Val Tyr Ile
 100 105 110

Asn Gly Ile Thr Tyr Thr Pro Val Ser Ser Thr Asn Glu Lys Asp Met
 115 120 125

Tyr Ser Phe Leu Glu Asp Met Gly Leu Lys Ala Phe Thr Asn Ser Lys
 130 135 140

Ile Arg Lys Pro Lys Met Cys Pro Gln Leu Gln Gln Tyr Glu Met His
 145 150 155 160

Gly Pro Glu Gly Leu Arg Val Gly Phe Tyr Glu Ser Asp Val Met Gly

465		470		475		480
Lys His Tyr Asp Gly Ser Tyr Ser Thr Phe Gly Glu Arg Tyr Gly Arg						
	485			490		495
Asn Gln Gly Asn Thr Trp Leu Thr Ala Phe Val Leu Lys Thr Phe Ala						
	500			505		510
Gln Ala Arg Ala Tyr Ile Phe Ile Asp Glu Ala His Ile Thr Gln Ala						
	515			520		525
Leu Ile Trp Leu Ser Gln Arg Gln Lys Asp Asn Gly Cys Phe Arg Ser						
	530			535		540
Ser Gly Ser Leu Leu Asn Asn Ala Ile Lys Gly Gly Val Glu Asp Glu						
	545			550		555
						560
Val Thr Leu Ser Ala Tyr Ile Thr Ile Ala Leu Leu Glu Ile Pro Leu						
				570		575
Thr Val Thr His Pro Val Val Arg Asn Ala Leu Phe Cys Leu Glu Ser						
	580			585		590
Ala Trp Lys Thr Ala Gln Glu Gly Asp His Gly Ser His Val Tyr Thr						
	595			600		605
Lys Ala Leu Leu Ala Tyr Ala Phe Ala Leu Ala Gly Asn Gln Asp Lys						
	610			615		620
Arg Lys Glu Val Leu Lys Ser Leu Asn Glu Glu Ala Val Lys Lys Asp						
	625			630		635
						640
Asn Ser Val His Trp Glu Arg Pro Gln Lys Pro Lys Ala Pro Val Gly						
	645			650		655
His Phe Tyr Glu Pro Gln Ala Pro Ser Ala Glu Val Glu Met Thr Ser						
	660			665		670
Tyr Val Leu Leu Ala Tyr Leu Thr Ala Gln Pro Ala Pro Thr Ser Glu						
	675			680		685
Asp Leu Thr Ser Ala Thr Asn Ile Val Lys Trp Ile Thr Lys Gln Gln						
	690			695		700
Asn Ala Gln Gly Gly Phe Ser Ser Thr Gln Asp Thr Val Val Ala Leu						
	705			710		715
						720
His Ala Leu Ser Lys Tyr Gly Ala Ala Thr Phe Thr Arg Thr Gly Lys						
	725			730		735
Ala Ala Gln Val Thr Ile Gln Ser Ser Gly Thr Phe Ser Ser Lys Phe						
	740			745		750
Gln Val Asp Asn Asn Asn Arg Leu Leu Leu Gln Gln Val Ser Leu Pro						
	755			760		765
Glu Leu Pro Gly Glu Tyr Ser Met Lys Val Thr Gly Glu Gly Cys Val						

770	775	780
Tyr Leu Gln Thr Ser Leu Lys Tyr Asn Ile Leu Pro Glu Lys Glu Glu 785 790 795 800		
Phe Pro Phe Ala Leu Gly Val Gln Thr Leu Pro Gln Thr Cys Asp Glu 805 810 815		
Pro Lys Ala His Thr Ser Phe Gln Ile Ser Leu Ser Val Ser Tyr Thr 820 825 830		
Gly Ser Arg Ser Ala Ser Asn Met Ala Ile Val Asp Val Lys Met Val 835 840 845		
Ser Gly Phe Ile Pro Leu Lys Pro Thr Val Lys Met Leu Glu Arg Ser 850 855 860		
Asn His Val Ser Arg Thr Glu Val Ser Ser Asn His Val Leu Ile Tyr 865 870 875 880		
Leu Asp Lys Val Ser Asn Gln Thr Leu Ser Leu Phe Phe Thr Val Leu 885 890 895		
Gln Asp Val Pro Val Arg Asp Leu Lys Pro Ala Ile Val Lys Val Tyr 900 905 910		
Asp Tyr Tyr Glu Thr Gly Glu Phe Ala Ile Ala Glu Tyr Asn Ala Pro 915 920 925		
Cys Ser Lys Asp Leu Gly Asn Ala 930 935		

<210> 36
 <211> 898
 <212> PRT
 <213> Homo sapiens

<400> 36

Arg Leu Leu Ile Tyr Ala Val Leu Pro Thr Gly Asp Val Ile Gly Asp 1 5 10 15
Ser Ala Lys Tyr Asp Val Glu Asn Cys Leu Ala Asn Lys Val Asp Leu 20 25 30
Ser Phe Ser Pro Ser Gln Ser Leu Pro Ala Ser His Ala His Leu Arg 35 40 45
Val Thr Ala Ala Pro Gln Ser Val Cys Ala Leu Arg Ala Val Asp Gln 50 55 60
Ser Val Leu Leu Met Lys Pro Asp Ala Glu Leu Ser Ala Ser Ser Val 65 70 75 80
Tyr Asn Leu Leu Pro Glu Lys Asp Leu Thr Gly Phe Pro Gly Pro Leu 85 90 95

Asn	Asp	Gln	Asp	Asp	Glu	Asp	Cys	Ile	Asn	Arg	His	Asn	Val	Tyr	Ile	100	105	110	
Asn	Gly	Ile	Thr	Tyr	Thr	Pro	Val	Ser	Ser	Thr	Asn	Glu	Lys	Asp	Met	115	120	125	
Tyr	Ser	Phe	Leu	Glu	Asp	Met	Gly	Leu	Lys	Ala	Phe	Thr	Asn	Ser	Lys	130	135	140	
Ile	Arg	Lys	Glu	Glu	Pro	His	Thr	Glu	Thr	Val	Arg	Lys	Tyr	Phe	Pro	145	150	155	160
Glu	Thr	Trp	Ile	Trp	Asp	Leu	Val	Val	Val	Asn	Ser	Ala	Gly	Val	Ala	165	170	175	
Glu	Val	Gly	Val	Thr	Val	Pro	Asp	Thr	Ile	Thr	Glu	Trp	Lys	Ala	Gly	180	185	190	
Ala	Phe	Cys	Leu	Ser	Glu	Asp	Ala	Gly	Leu	Gly	Ile	Ser	Ser	Thr	Ala	195	200	205	
Ser	Leu	Arg	Ala	Phe	Gln	Pro	Phe	Phe	Val	Glu	Leu	Thr	Met	Pro	Tyr	210	215	220	
Ser	Val	Ile	Arg	Gly	Glu	Ala	Phe	Thr	Leu	Lys	Ala	Thr	Val	Leu	Asn	225	230	235	240
Tyr	Leu	Pro	Lys	Cys	Ile	Arg	Val	Ser	Val	Gln	Leu	Glu	Ala	Ser	Pro	245	250	255	
Ala	Phe	Leu	Ala	Val	Pro	Val	Glu	Lys	Glu	Gln	Ala	Pro	His	Cys	Ile	260	265	270	
Cys	Ala	Asn	Gly	Arg	Gln	Thr	Val	Ser	Trp	Ala	Val	Thr	Pro	Lys	Ser	275	280	285	
Leu	Gly	Asn	Val	Asn	Phe	Thr	Val	Ser	Ala	Glu	Ala	Leu	Glu	Ser	Gln	290	295	300	
Glu	Leu	Cys	Gly	Thr	Glu	Val	Pro	Ser	Val	Pro	Glu	His	Gly	Arg	Lys	305	310	315	320
Asp	Thr	Val	Ile	Lys	Pro	Leu	Leu	Val	Glu	Pro	Glu	Gly	Leu	Glu	Lys	325	330	335	
Glu	Thr	Thr	Phe	Asn	Ser	Leu	Leu	Cys	Pro	Ser	Gly	Gly	Glu	Val	Ser	340	345	350	
Glu	Glu	Leu	Ser	Leu	Lys	Leu	Pro	Pro	Asn	Val	Val	Glu	Glu	Ser	Ala	355	360	365	
Arg	Ala	Ser	Val	Ser	Val	Leu	Gly	Asp	Ile	Leu	Gly	Ser	Ala	Met	Gln	370	375	380	
Asn	Thr	Gln	Asn	Leu	Leu	Gln	Met	Pro	Tyr	Gly	Cys	Gly	Glu	Gln	Asn	385	390	395	400

Met Val Leu Phe Ala Pro Asn Ile Tyr Val Leu Asp Tyr Leu Asn Glu
 405 410 415
 Thr Gln Gln Leu Thr Pro Glu Val Lys Ser Lys Ala Ile Gly Tyr Leu
 420 425 430
 Asn Thr Gly Tyr Gln Arg Gln Leu Asn Tyr Lys His Tyr Asp Gly Ser
 435 440 445
 Tyr Ser Thr Phe Gly Glu Arg Tyr Gly Arg Asn Gln Gly Asn Thr Trp
 450 455 460
 Leu Thr Ala Phe Val Leu Lys Thr Phe Ala Gln Ala Arg Ala Tyr Ile
 465 470 475 480
 Phe Ile Asp Glu Ala His Ile Thr Gln Ala Leu Ile Trp Leu Ser Gln
 485 490 495
 Arg Gln Lys Asp Asn Gly Cys Phe Arg Ser Ser Gly Ser Leu Leu Asn
 500 505 510
 Asn Ala Ile Lys Gly Gly Val Glu Asp Glu Val Thr Leu Ser Ala Tyr
 515 520 525
 Ile Thr Ile Ala Leu Leu Glu Ile Pro Leu Thr Val Thr His Pro Val
 530 535 540
 Val Arg Asn Ala Leu Phe Cys Leu Glu Ser Ala Trp Lys Thr Ala Gln
 545 550 555 560
 Glu Gly Asp His Gly Ser His Val Tyr Thr Lys Ala Leu Leu Ala Tyr
 565 570 575
 Ala Phe Ala Leu Ala Gly Asn Gln Asp Lys Arg Lys Glu Val Leu Lys
 580 585 590
 Ser Leu Asn Glu Glu Ala Val Lys Lys Asp Asn Ser Val His Trp Glu
 595 600 605
 Arg Pro Gln Lys Pro Lys Ala Pro Val Gly His Phe Tyr Glu Pro Gln
 610 615 620
 Ala Pro Ser Ala Glu Val Glu Met Thr Ser Tyr Val Leu Leu Ala Tyr
 625 630 635 640
 Leu Thr Ala Gln Pro Ala Pro Thr Ser Glu Asp Leu Thr Ser Ala Thr
 645 650 655
 Asn Ile Val Lys Trp Ile Thr Lys Gln Gln Asn Ala Gln Gly Gly Phe
 660 665 670
 Ser Ser Thr Gln Asp Thr Val Val Ala Leu His Ala Leu Ser Lys Tyr
 675 680 685
 Gly Ala Ala Thr Phe Thr Arg Thr Gly Lys Ala Ala Gln Val Thr Ile
 690 695 700

Gln Ser Ser Gly Thr Phe Ser Ser Lys Phe Gln Val Asp Asn Asn Asn
 705 710 715 720
 Arg Leu Leu Leu Gln Gln Val Ser Leu Pro Glu Leu Pro Gly Glu Tyr
 725 730 735
 Ser Met Lys Val Thr Gly Glu Gly Cys Val Tyr Leu Gln Thr Ser Leu
 740 745 750
 Lys Tyr Asn Ile Leu Pro Glu Lys Glu Glu Phe Pro Phe Ala Leu Gly
 755 760 765
 Val Gln Thr Leu Pro Gln Thr Cys Asp Glu Pro Lys Ala His Thr Ser
 770 775 780
 Phe Gln Ile Ser Leu Ser Val Ser Tyr Thr Gly Ser Arg Ser Ala Ser
 785 790 795 800
 Asn Met Ala Ile Val Asp Val Lys Met Val Ser Gly Phe Ile Pro Leu
 805 810 815
 Lys Pro Thr Val Lys Met Leu Glu Arg Ser Asn His Val Ser Arg Thr
 820 825 830
 Glu Val Ser Ser Asn His Val Leu Ile Tyr Leu Asp Lys Val Ser Asn
 835 840 845
 Gln Thr Leu Ser Leu Phe Phe Thr Val Leu Gln Asp Val Pro Val Arg
 850 855 860
 Asp Leu Lys Pro Ala Ile Val Lys Val Tyr Asp Tyr Tyr Glu Thr Asp
 865 870 875 880
 Glu Phe Ala Ile Ala Glu Tyr Asn Ala Pro Cys Ser Lys Asp Leu Gly
 885 890 895

Asn Ala

<210> 37
 <211> 936
 <212> PRT
 <213> Homo sapiens

<400> 37
 Arg Leu Leu Ile Tyr Ala Val Leu Pro Thr Gly Asp Val Ile Gly Asp
 1 5 10 15
 Ser Ala Lys Tyr Asp Val Glu Asn Glu Leu Ala Asn Lys Val Asp Leu
 20 25 30
 Ser Phe Ser Pro Ser Gln Ser Leu Pro Ala Ser His Ala His Leu Arg
 35 40 45
 Val Thr Ala Ala Pro Gln Ser Val Cys Ala Leu Arg Ala Val Asp Gln
 50 55 60

Ser Val Leu Leu Met Lys Pro Asp Ala Glu Leu Ser Ala Ser Ser Val
 65 70 75 80
 Tyr Asn Leu Leu Pro Glu Lys Asp Leu Thr Gly Phe Pro Gly Pro Leu
 85 90 95
 Asn Asp Gln Asp Asp Glu Asp Cys Ile Asn Arg His Asn Val Tyr Ile
 100 105 110
 Asn Gly Ile Thr Tyr Thr Pro Val Ser Ser Thr Asn Glu Lys Asp Met
 115 120 125
 Tyr Ser Phe Leu Glu Asp Met Gly Leu Lys Ala Phe Thr Asn Ser Lys
 130 135 140
 Ile Arg Lys Pro Lys Met Cys Pro Gln Leu Gln Gln Tyr Glu Met His
 145 150 155 160
 Gly Pro Glu Gly Leu Arg Val Gly Phe Tyr Glu Ser Asp Val Met Gly
 165 170 175
 Arg Gly His Ala Arg Leu Val His Val Glu Glu Pro His Thr Glu Thr
 180 185 190
 Val Arg Lys Tyr Phe Pro Glu Thr Trp Ile Trp Asp Leu Val Val Val
 195 200 205
 Asn Ser Ala Gly Val Ala Glu Val Gly Val Thr Val Pro Asp Thr Ile
 210 215 220
 Thr Glu Trp Lys Ala Gly Ala Phe Cys Leu Ser Glu Asp Ala Gly Leu
 225 230 235 240
 Gly Ile Ser Ser Thr Ala Ser Leu Arg Ala Phe Gln Pro Phe Phe Val
 245 250 255
 Glu Leu Thr Met Pro Tyr Ser Val Ile Arg Gly Glu Ala Phe Thr Leu
 260 265 270
 Lys Ala Thr Val Leu Asn Tyr Leu Pro Lys Cys Ile Arg Val Ser Val
 275 280 285
 Gln Leu Glu Ala Ser Pro Ala Phe Leu Ala Val Pro Val Glu Lys Glu
 290 295 300
 Gln Ala Pro His Cys Ile Cys Ala Asn Gly Arg Gln Thr Val Ser Trp
 305 310 315 320
 Ala Val Thr Pro Lys Ser Leu Gly Asn Val Asn Phe Thr Val Ser Ala
 325 330 335
 Glu Ala Leu Glu Ser Gln Glu Leu Cys Gly Thr Glu Val Pro Ser Val
 340 345 350
 Pro Glu His Gly Arg Lys Asp Thr Val Ile Lys Pro Leu Leu Val Glu
 355 360 365

Pro Glu Gly Leu Glu Lys Glu Thr Thr Phe Asn Ser Leu Leu Cys Pro
 370 375 380
 Ser Gly Gly Glu Val Ser Glu Glu Leu Ser Leu Lys Leu Pro Pro Asn
 385 390 395 400
 Val Val Glu Glu Ser Ala Arg Ala Ser Val Ser Val Leu Gly Asp Ile
 405 410 415
 Leu Gly Ser Ala Met Gln Asn Thr Gln Asn Leu Leu Gln Met Pro Tyr
 420 425 430
 Gly Cys Gly Glu Glx Asn Met Val Leu Phe Ala Pro Asn Ile Tyr Val
 435 440 445
 Leu Asp Tyr Leu Asn Glu Thr Gln Gln Leu Thr Pro Glu Ile Lys Ser
 450 455 460
 Lys Ala Ile Gly Tyr Leu Asn Thr Gly Tyr Gln Arg Gln Leu Asn Tyr
 465 470 475 480
 Lys His Tyr Asp Gly Ser Tyr Ser Thr Phe Gly Glu Arg Tyr Gly Arg
 485 490 495
 Asn Gln Gly Asn Thr Trp Leu Thr Ala Phe Val Leu Lys Thr Phe Ala
 500 505 510
 Gln Ala Arg Ala Tyr Ile Phe Ile Asp Glu Ala His Ile Thr Gln Ala
 515 520 525
 Leu Ile Trp Leu Ser Gln Arg Gln Lys Asp Asn Gly Cys Phe Arg Ser
 530 535 540
 Ser Gly Ser Leu Leu Asn Asn Ala Ile Lys Gly Gly Val Glu Asp Glu
 545 550 555 560
 Val Thr Leu Ser Ala Tyr Ile Lys Ile Ala Leu Leu Glu Ile Pro Leu
 565 570 575
 Thr Val Thr His Pro Val Val Arg Asn Ala Leu Phe Cys Leu Glu Ser
 580 585 590
 Ala Trp Lys Thr Ala Glu Glu Gly Asp His Gly Ser His Val Tyr Thr
 595 600 605
 Lys Ala Leu Leu Ala Tyr Ala Phe Ala Leu Ala Gly Asn Gln Asp Lys
 610 615 620
 Arg Lys Glu Val Leu Lys Ser Leu Asn Glu Glu Ala Val Lys Lys Asp
 625 630 635 640
 Asn Ser Val His Trp Glu Arg Pro Gln Lys Pro Lys Ala Pro Val Gly
 645 650 655
 His Phe Tyr Glu Pro Gln Ala Pro Ser Ala Glu Val Glu Met Thr Ser
 660 665 670

Tyr Val Leu Leu Ala Tyr Leu Thr Ala Gln Pro Ala Pro Thr Ser Glu
 675 680 685
 Asp Leu Thr Ser Ala Thr Asn Ile Val Lys Trp Ile Thr Lys Gln Gln
 690 695 700
 Asn Ala Gln Gly Gly Phe Ser Ser Thr Gln Asp Lys Val Val Ala Leu
 705 710 715 720
 His Ala Leu Ser Lys Tyr Gly Ala Ala Thr Phe Thr Arg Thr Gly Lys
 725 730 735
 Ala Ala Gln Val Thr Ile Gln Ser Ser Gly Thr Phe Ser Ser Lys Phe
 740 745 750
 Gln Val Asp Asn Asn Asn Arg Leu Leu Leu Gln Gln Val Ser Leu Pro
 755 760 765
 Glu Leu Pro Gly Glu Tyr Ser Met Lys Val Thr Gly Glu Gly Cys Val
 770 775 780
 Tyr Leu Gln Thr Ser Leu Lys Tyr Asn Ile Leu Pro Glu Lys Glu Glu
 785 790 795 800
 Phe Pro Phe Ala Leu Gly Val Gln Thr Leu Pro Gln Thr Cys Asp Glu
 805 810 815
 Pro Lys Ala His Thr Ser Phe Gln Ile Ser Leu Ser Val Ser Tyr Thr
 820 825 830
 Gly Ser Arg Ser Ala Ser Asn Met Ala Ile Val Asp Val Lys Met Val
 835 840 845
 Ser Gly Phe Ile Pro Leu Lys Pro Thr Val Lys Met Leu Glu Arg Ser
 850 855 860
 Asn His Val Ser Arg Thr Glu Val Ser Ser Asn His Val Leu Ile Tyr
 865 870 875 880
 Leu Asp Lys Val Ser Asn Gln Thr Leu Ser Leu Phe Phe Thr Val Leu
 885 890 895
 Gln Asp Val Pro Val Arg Asp Leu Lys Pro Ala Ile Val Lys Val Tyr
 900 905 910
 Asp Tyr Tyr Glu Thr Asp Glu Phe Ala Ile Ala Glu Tyr Asn Ala Pro
 915 920 925
 Cys Ser Lys Asp Leu Gly Asn Ala
 930 935

<210> 38
 <211> 931
 <212> PRT
 <213> Rattus norvegicus

<400> 38

Arg	Leu	Val	Leu	Tyr	Ala	Ile	Leu	Pro	Asn	Gly	Glu	Val	Val	Gly	Asp	
1				5					10					15		
Thr	Ala	Lys	Tyr	Glu	Ile	Glu	Asn	Cys	Leu	Ala	Asn	Lys	Val	Asp	Leu	
			20					25					30			
Val	Phe	Arg	Pro	Asn	Ser	Gly	Leu	Pro	Ala	Thr	Arg	Ala	Leu	Leu	Ser	
		35					40					45				
Val	Met	Ala	Ser	Pro	Gln	Ser	Leu	Cys	Gly	Leu	Arg	Ala	Val	Asp	Gln	
	50					55					60					
Ser	Val	Leu	Leu	Met	Lys	Pro	Glu	Thr	Glu	Leu	Ser	Ala	Ser	Leu	Ile	
65					70					75					80	
Tyr	Asp	Leu	Leu	Pro	Val	Lys	Asp	Leu	Thr	Gly	Phe	Pro	Gln	Gly	Ala	
				85					90					95		
Asp	Gln	Arg	Glu	Glu	Asp	Thr	Asn	Gly	Cys	Val	Lys	Gln	Asn	Asp	Thr	
			100					105					110			
Tyr	Ile	Asn	Gly	Ile	Leu	Tyr	Ser	Pro	Val	Gln	Asn	Thr	Asn	Glu	Glu	
	115						120					125				
Asp	Met	Tyr	Gly	Phe	Leu	Lys	Asp	Met	Gly	Leu	Lys	Val	Phe	Thr	Asn	
	130					135					140					
Ser	Asn	Ile	Arg	Lys	Pro	Lys	Val	Cys	Glu	Arg	Leu	Arg	Asp	Asn	Lys	
145					150				155						160	
Gly	Ile	Pro	Ala	Ala	Tyr	His	Leu	Val	Ser	Gln	Ser	His	Met	Asp	Ala	
			165					170						175		
Phe	Leu	Glu	Ser	Ser	Glu	Ser	Pro	Thr	Glu	Thr	Arg	Arg	Ser	Tyr	Phe	
			180					185					190			
Pro	Glu	Thr	Trp	Ile	Trp	Asp	Leu	Val	Val	Val	Asp	Ser	Ala	Gly	Val	
		195					200					205				
Ala	Glu	Val	Glu	Val	Thr	Val	Pro	Asp	Thr	Ile	Thr	Glu	Trp	Lys	Ala	
	210					215					220					
Gly	Ala	Phe	Cys	Leu	Ser	Asn	Asp	Thr	Gly	Leu	Gly	Leu	Ser	Pro	Val	
225					230					235					240	
Val	Gln	Phe	Gln	Ala	Phe	Gln	Pro	Phe	Phe	Val	Glu	Leu	Thr	Met	Pro	
			245						250					255		
Tyr	Ser	Val	Ile	Arg	Gly	Glu	Ala	Phe	Thr	Leu	Lys	Ala	Thr	Val	Leu	
			260					265					270			
Asn	Tyr	Leu	Pro	Thr	Cys	Ile	Arg	Val	Ala	Val	Gln	Leu	Glu	Ala	Ser	
	275						280					285				
Pro	Asp	Phe	Leu	Ala	Ala	Pro	Glu	Glu	Lys	Glu	Gln	Arg	Ser	His	Cys	

290	295	300
Ile Cys Met Asn Gln Arg His Thr Ala Ser Trp Ala Val Ile Pro Lys 305 310 315 320		
Ser Leu Gly Asn Val Asn Phe Thr Val Ser Ala Glu Ala Leu Asn Ser 325 330 335		
Lys Glu Leu Cys Gly Asn Glu Val Pro Val Val Pro Glu Gln Gly Lys 340 345 350		
Lys Asp Thr Ile Ile Lys Ser Leu Leu Val Glu Pro Glu Gly Leu Glu 355 360 365		
Asn Glu Val Thr Phe Asn Ser Leu Leu Cys Pro Met Gly Ala Glu Val 370 375 380		
Ser Glu Leu Ile Ala Leu Lys Leu Pro Ser Asp Val Val Glu Glu Ser 385 390 395 400		
Ala Arg Ala Ser Val Thr Val Leu Gly Asp Ile Leu Gly Ser Ala Met 405 410 415		
Gln Asn Thr Gln Asp Leu Leu Lys Met Pro Tyr Gly Cys Gly Glu Gln 420 425 430		
Asn Met Val Leu Phe Ala Pro Asn Ile Tyr Val Leu Asp Tyr Leu Asn 435 440 445		
Glu Thr Gln Gln Leu Thr Gln Glu Ile Lys Thr Lys Ala Ile Ala Tyr 450 455 460		
Leu Asn Thr Gly Tyr Gln Arg Gln Leu Asn Tyr Lys His Arg Asp Gly 465 470 475 480		
Ser Tyr Ser Ala Phe Gly Asp Lys Pro Gly Arg Asn His Ala Asn Thr 485 490 495		
Trp Leu Thr Ala Phe Val Leu Lys Ser Phe Ala Gln Ala Arg Lys Tyr 500 505 510		
Ile Phe Ile Asp Glu Val His Ile Thr Gln Ala Leu Leu Trp Leu Ser 515 520 525		
Gln Gln Gln Lys Asp Asn Gly Cys Phe Arg Ser Ser Gly Ser Leu Leu 530 535 540		
Asn Asn Ala Met Lys Gly Gly Val Glu Asp Glu Val Thr Leu Ser Ala 545 550 555 560		
Tyr Ile Thr Ile Ala Leu Leu Glu Met Ser Leu Pro Val Thr His Pro 565 570 575		
Val Val Arg Asn Ala Leu Phe Cys Leu Asp Thr Ala Trp Lys Ser Ala 580 585 590		
Arg Gly Gly Ala Gly Gly Ser His Val Tyr Thr Lys Ala Leu Leu Ala		

595	600	605
Tyr Ala Phe Ala Leu Ala Gly Pro Val Val Arg Asn Ala Leu Phe Cys 610 615 620		
Leu Asp Thr Ala Trp Lys Ser Ala Arg Gly Gly Ala Gly Gly Ser His 625 630 635 640		
Val Tyr Thr Lys Ala Leu Leu Ala Tyr Ala Phe Ala Leu Ala Gly Pro 645 650 655		
Gln Ala Thr Ser Ala Glu Val Glu Met Thr Ala Tyr Val Leu Leu Ala 660 665 670		
Tyr Leu Thr Thr Glu Pro Ala Pro Thr Gln Glu Asp Leu Thr Ala Ala 675 680 685		
Met Leu Ile Val Lys Trp Leu Thr Lys Gln Gln Asn Ser His Gly Gly 690 695 700		
Phe Ser Ser Thr Gln Asp Thr Val Val Ala Leu His Ala Leu Ser Lys 705 710 715 720		
Tyr Gly Ser Ala Thr Phe Thr Arg Ala Lys Lys Ala Ala Gln Val Thr 725 730 735		
Ile Arg Ser Ser Gly Thr Phe Ser Thr Lys Phe Gln Val Asn Asn Asn 740 745 750		
Asn Gln Leu Leu Leu Gln Arg Val Thr Leu Pro Thr Val Pro Gly Asp 755 760 765		
Tyr Thr Val Lys Val Thr Gly Glu Gly Cys Val Tyr Leu Gln Thr Ser 770 775 780		
Leu Lys Tyr Ser Val Leu Pro Arg Glu Glu Glu Phe Pro Phe Ala Val 785 790 795 800		
Val Val Gln Thr Leu Pro Gly Thr Cys Glu Asp Pro Lys Ala His Thr 805 810 815		
Ser Phe Gln Ile Ser Leu Asn Ile Ser Tyr Thr Gly Ser Arg Ser Glu 820 825 830		
Ser Asn Met Ala Ile Ala Asp Val Lys Met Val Ser Gly Phe Ile Pro 835 840 845		
Leu Lys Pro Thr Val Lys Met Leu Glu Arg Ser Val His Val Ser Arg 850 855 860		
Thr Glu Val Ser Asn Asn His Val Leu Ile Tyr Leu Asp Lys Val Ser 865 870 875 880		
Asn Gln Thr Val Asn Leu Ser Phe Thr Val Gln Gln Asp Ile Pro Ile 885 890 895		
Arg Asp Leu Lys Pro Ala Val Val Lys Val Tyr Asp Tyr Tyr Glu Lys		

900	905	910
Asp Glu Phe Ala Val Ala Lys Tyr Ser Ala Pro Cys Ser Thr Asp Tyr		
915	920	925
Gly Asn Ala		
930		
<210> 39		
<211> 941		
<212> PRT		
<213> Cavia porcellus		
<400> 39		
Arg Val Leu Ile Tyr Ala Ile Leu Pro Ser Gly Glu Ile Ile Ala Asp		
1	5	10 15
Ser Ala Lys Tyr Asn Val Glu Asn Cys Leu Asp Asn Lys Val Asn Leu		
20	25	30
Ser Phe Ser Glu Gly Gln Ser Leu Pro Ala Ser Lys Thr His Leu Arg		
35	40	45
Val Thr Ala Ser Pro Gln Ser Leu Cys Ala Leu Arg Ala Val Asp Gln		
50	55	60
Ser Val Leu Leu Arg Lys Pro Glu Ala Val Leu Ser Ala Ser Ser Val		
65	70	75 80
Tyr Ala Leu Leu Pro Val Lys Asp Leu Thr Gly Phe Pro Gly Leu Leu		
85	90	95
Gly Gln Gln Glu Glu Asn Asp Gly Glu Cys Val Ser Leu Tyr Asn Thr		
100	105	110
Tyr Ile Asp Gly Ile Leu Tyr Ser Pro Glu Pro Asn Ile Asn Glu Lys		
115	120	125
Asp Met Tyr Gly Phe Leu Lys Asp Met Gly Leu Lys Val Phe Thr Asn		
130	135	140
Thr Lys Ile Gln Lys Pro Gln Leu Cys Ala His Val Gln Lys Phe Glu		
145	150	155 160
Val Pro Thr Met Ala Tyr Ser Tyr Ser Glu Ser Ser Ser Phe Arg Ser		
165	170	175
Gly Pro Arg Arg Val Pro Ala Val Gly Ile Ala Ala Thr Tyr Ser Glu		
180	185	190
Pro Pro Lys Glu Thr Val Arg Thr Tyr Ser Pro Glu Thr Trp Ile Trp		
195	200	205
Asp Leu Lys Val Thr Asp Ser Ser Gly Val Ala Glu Val Glu Val Thr		
210	215	220

Val Pro Asp Thr Ile Thr Glu Trp Lys Ala Gly Ala Phe Cys Leu Ser
 225 230 235 240
 Asn Asp Thr Gly Leu Gly Leu Ser Pro Thr Ala Ser Leu Arg Ala Phe
 245 250 255
 Gln Pro Phe Phe Val Glu Leu Thr Met Pro Tyr Ser Val Ile Arg Gly
 260 265 270
 Glu Ala Phe Thr Leu Lys Ala Thr Val Leu Asn Tyr Leu Pro Asp Cys
 275 280 285
 Ile Arg Ile Ser Val His Leu Glu Ala Ser Pro Lys Phe Leu Ala Glu
 290 295 300
 Pro Lys Ala Lys Glu Gln Glu Ser Tyr Cys Val Cys Gly Asn Glu Arg
 305 310 315 320
 Gln Thr Val Ser Trp Val Val Thr Pro Lys Ser Leu Gly Asn Val Asn
 325 330 335
 Phe Thr Val Ser Ala Glu Ala Leu Glu Ser Ser Glu Leu Cys Gly Asn
 340 345 350
 Glu Lys Thr Val Val Pro Thr Tyr Gly Lys Lys Asp Thr Ile Ile Lys
 355 360 365
 Pro Leu Leu Val Glu Pro Glu Gly Ile Glu Lys Glu Glu Thr Trp Thr
 370 375 380
 Ser Leu Ile Arg Val Ser Asp Thr Thr Val Ser Glu Lys Leu His Leu
 385 390 395 400
 Glu Leu Pro Ser Asn Val Ile Gln Asp Ser Ala Arg Ala Thr Val Ser
 405 410 415
 Ile Leu Gly Asp Ile Leu Gly Ser Ala Met Gln Asn Ile Gln Asn Leu
 420 425 430
 Leu Gln Met Pro Tyr Gly Cys Gly Glu Gln Asn Met Val Leu Phe Ala
 435 440 445
 Pro Asn Ile Tyr Val Leu Asp Tyr Leu Asn Glu Thr Gln Gln Leu Thr
 450 455 460
 Pro Asp Ile Lys Ser Lys Ala Ile Ser Tyr Leu Ser Thr Gly Tyr Gln
 465 470 475 480
 Arg Gln Leu Asn Tyr Lys His Arg Asp Gly Ser Tyr Ser Thr Phe Gly
 485 490 495
 Glu Asn Tyr Arg Gly Gly Gln Gly Asn Thr Trp Leu Thr Ala Phe Val
 500 505 510
 Leu Lys Thr Phe Ser Gln Ala Arg Lys Tyr Ile Phe Ile Asp Glu Ala
 515 520 525

His Ile Thr Gln Ala Leu Ser Trp Leu Ser Gln Lys Gln Lys Asp Asn
 530 535 540

Gly Cys Phe Trp Ser Ser Gly Ser Leu Leu Asn Asn Ala Ile Lys Gly
 545 550 555 560

Gly Val Glu Asp Glu Ile Ser Leu Ser Ala Tyr Ile Thr Ile Ala Leu
 565 570 575

Leu Glu Met Ser Leu Pro Asp Thr His Pro Val Val Arg Asn Ala Leu
 580 585 590

Phe Cys Leu Glu Ser Ala Trp Lys Ser Ala Lys Glu Gly Thr His Gly
 595 600 605

Ser His Val Tyr Thr Lys Ala Leu Leu Ala Tyr Ala Phe Ala Leu Ala
 610 615 620

Gly Asn Gln Glu Arg Lys Lys Glu Ile Leu Lys Ser Leu Glu Asp Glu
 625 630 635 640

Gly Val Lys Glu Asp Asn Ser Leu His Trp Ala Arg Pro Gln Lys Pro
 645 650 655

Lys Val Ser Glu Gly Phe Leu Phe Lys Ser Gln Ala Pro Ser Ala Glu
 660 665 670

Val Glu Met Thr Ser Tyr Val Leu Leu Ala Tyr Leu Thr Ala Arg Pro
 675 680 685

Ala Pro Thr Pro Glu Asp Leu Thr Ser Ala Thr Asp Ile Val Asn Trp
 690 695 700

Val Thr Lys Gln Gln Asn Ser His Gly Gly Tyr Ser Ser Thr Gln Asp
 705 710 715 720

Thr Val Val Ala Leu His Ala Leu Ser Lys Tyr Ala Ala Ala Thr Phe
 725 730 735

Thr Arg Thr Glu Lys Ala Ala Gln Val Thr Ile Lys Ser Ser Gly Thr
 740 745 750

Phe Ser Thr Asn Phe Glu Val Asn His Asn Asn Arg Leu Leu Leu Gln
 755 760 765

Gln Val Ser Leu Pro Thr Val Ser Asp Ser Tyr Thr Ile Thr Val Thr
 770 775 780

Gly Glu Gly Asn Val Tyr Leu Gln Thr Ser Leu Lys Tyr Asn Val Pro
 785 790 795 800

Ser Glu Lys Gly Thr Phe Pro Phe Ala Leu Glu Ala Glu Thr Val Pro
 805 810 815

Gln Ala Cys Asp Gly Pro Lys Ala His Thr Ser Phe Gln Ile Ser Leu
 820 825 830

Asn Val Ser Tyr Ile Gly Ser Arg Pro Val Ser Asn Met Ala Ile Val
835 840 845

Asp Val Lys Met Val Ser Gly Phe Ile Pro Leu Lys Pro Thr Val Lys
850 855 860

Asn Leu Glu Lys Ser Glu His Ile Ser Arg Thr Glu Val Ser Asn Asn
865 870 875 880

His Val Leu Ile Tyr Leu Asp Lys Val Ser Asn Gln Thr Leu Ser Leu
885 890 895

Ser Phe Phe Val Val Gln Asp Ile Glu Val Arg Asp Leu Lys Pro Ala
900 905 910

Ile Ile Lys Val Tyr Asp Tyr Tyr Glu Thr Asn Glu Phe Ala Ile Ala
915 920 925

Glu Tyr His Ala Pro Cys Ser Lys Asp Pro Gly Asn Ala
930 935 940

<210> 40

<211> 373

<212> PRT

<213> Mus musculus

<400> 40

Met Ser Thr Asp Cys Ala Gly Asn Ser Thr Cys Pro Val Asn Ser Thr
1 5 10 15

Glu Glu Asp Pro Pro Val Gly Met Glu Gly His Ala Asn Leu Lys Leu
20 25 30

Leu Phe Thr Val Leu Ser Ala Val Met Val Gly Leu Val Met Phe Ser
35 40 45

Phe Gly Cys Ser Val Glu Ser Gln Lys Leu Trp Leu His Leu Arg Arg
50 55 60

Pro Trp Gly Ile Ala Val Gly Leu Leu Ser Gln Phe Gly Leu Met Pro
65 70 75 80

Leu Thr Ala Tyr Leu Leu Ala Ile Gly Phe Gly Leu Lys Pro Phe Gln
85 90 95

Ala Ile Ala Val Leu Met Met Gly Ser Cys Pro Gly Gly Thr Ile Ser
100 105 110

Asn Val Leu Thr Phe Trp Val Asp Gly Asp Met Asp Leu Ser Ile Ser
115 120 125

Met Thr Thr Cys Ser Thr Val Ala Ala Leu Gly Met Met Pro Leu Cys
130 135 140

Leu Tyr Ile Tyr Thr Arg Ser Trp Thr Leu Thr Gln Asn Leu Val Ile
145 150 155 160

Pro Tyr Gln Ser Ile Gly Ile Thr Leu Val Ser Leu Val Val Pro Val
165 170 175

Ala Ser Gly Val Tyr Val Asn Tyr Arg Trp Pro Lys Gln Ala Thr Val
180 185 190

Ile Leu Lys Val Gly Ala Ile Leu Gly Gly Met Leu Leu Leu Val Val
195 200 205

Ala Val Thr Gly Met Val Leu Ala Lys Gly Trp Asn Thr Asp Val Thr
210 215 220

Leu Leu Val Ile Ser Cys Ile Phe Pro Leu Val Gly His Val Thr Gly
225 230 235 240

Phe Leu Leu Ala Phe Leu Thr His Gln Ser Trp Gln Arg Cys Arg Thr
245 250 255

Ile Ser Ile Glu Thr Gly Ala Gln Asn Ile Gln Leu Cys Ile Ala Met
260 265 270

Leu Gln Leu Ser Phe Ser Ala Glu Tyr Leu Val Gln Leu Leu Asn Phe
275 280 285

Ala Leu Ala Tyr Gly Leu Phe Gln Val Leu His Gly Leu Leu Ile Val
290 295 300

Ala Ala Tyr Gln Ala Tyr Lys Arg Arg Gln Lys Ser Lys Cys Arg Arg
305 310 315 320

Gln His Pro Asp Cys Pro Asp Val Cys Tyr Glu Lys Gln Pro Arg Glu
325 330 335

Thr Ser Ala Phe Leu Asp Lys Gly Asp Glu Ala Ala Val Thr Leu Gly
340 345 350

Pro Val Gln Pro Glu Gln His His Arg Ala Ala Glu Leu Thr Ser His
355 360 365

Ile Pro Ser Cys Glu
370

<210> 41

<211> 347

<212> PRT

<213> *Oryzctolagus cuniculus*

<400> 41

Met Ser Asn Leu Thr Val Gly Cys Leu Ala Asn Ala Thr Val Cys Glu
1 5 10 15

Gly Ala Ser Cys Val Ala Pro Glu Ser Asn Phe Asn Ala Ile Leu Ser
20 25 30

Val Val Leu Ser Thr Val Leu Thr Ile Leu Leu Ala Leu Val Met Phe

35	40	45
Ser Met Gly Cys Asn Val Glu Ile Lys Lys Phe Leu Gly His Ile Arg		
50	55	60
Arg Pro Trp Gly Ile Phe Ile Gly Phe Leu Cys Gln Phe Gly Ile Met		
65	70	75
Pro Leu Thr Gly Phe Val Leu Ala Val Ala Phe Gly Ile Met Pro Ile		
85	90	95
Gln Ala Val Val Val Leu Ile Met Gly Cys Cys Pro Gly Gly Thr Ala		
100	105	110
Ser Asn Ile Leu Ala Tyr Trp Val Asp Gly Asp Met Asp Leu Ser Val		
115	120	125
Ser Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu		
130	135	140
Cys Leu Tyr Val Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val		
145	150	155
Ile Pro Tyr Asp Asn Ile Gly Thr Ser Leu Val Ala Leu Val Val Pro		
165	170	175
Val Ser Ile Gly Met Phe Val Asn His Lys Trp Pro Gln Lys Ala Lys		
180	185	190
Ile Ile Leu Lys Val Gly Ser Ile Ala Gly Ala Val Leu Ile Val Leu		
195	200	205
Ile Ala Val Val Gly Gly Ile Leu Tyr Gln Ser Ala Trp Ile Ile Glu		
210	215	220
Pro Lys Leu Trp Ile Ile Gly Thr Ile Phe Pro Met Ala Gly Tyr Ser		
225	230	235
Leu Gly Phe Phe Leu Ala Arg Ile Ala Gly Gln Pro Trp Tyr Arg Cys		
245	250	255
Arg Thr Val Ala Leu Glu Thr Gly Met Gln Asn Thr Gln Leu Cys Ser		
260	265	270
Thr Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Thr Tyr Val Phe		
275	280	285
Thr Phe Pro Leu Ile Tyr Ser Ile Phe Gln Ile Ala Phe Ala Ala Ile		
290	295	300
Phe Leu Gly Ile Tyr Val Ala Tyr Arg Lys Cys His Gly Lys Asn Asp		
305	310	315
Ala Glu Phe Pro Asp Ile Lys Asp Thr Lys Thr Glu Pro Glu Ser Ser		
325	330	335
Phe His Gln Met Asn Gly Gly Phe Gln Pro Glu		

340

345

<210> 42

<211> 348

<212> PRT

<213> Rattus norvegicus

<400> 42

Met Asp Asn Ser Ser Val Cys Ser Pro Asn Ala Thr Phe Cys Glu Gly
 1 5 10 15

Asp Ser Cys Leu Val Thr Glu Ser Asn Phe Asn Ala Ile Leu Ser Thr
 20 25 30

Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Met Val Met Phe Ser
 35 40 45

Met Gly Cys Asn Val Glu Ile Asn Lys Phe Leu Gly His Ile Lys Arg
 50 55 60

Pro Trp Gly Ile Phe Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro
 65 70 75 80

Leu Thr Gly Phe Ile Leu Ser Val Ala Ser Gly Ile Leu Pro Val Gln
 85 90 95

Ala Val Val Val Leu Ile Met Gly Cys Cys Pro Gly Gly Thr Gly Ser
 100 105 110

Asn Ile Leu Ala Tyr Trp Ile Asp Gly Asp Met Asp Leu Ser Val Ser
 115 120 125

Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu Cys
 130 135 140

Leu Phe Ile Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val Ile
 145 150 155 160

Pro Tyr Asp Ser Ile Gly Ile Ser Leu Val Ala Leu Val Ile Pro Val
 165 170 175

Ser Ile Gly Met Phe Val Asn His Lys Trp Pro Gln Lys Ala Lys Ile
 180 185 190

Ile Leu Lys Ile Gly Ser Ile Ala Gly Ala Ile Leu Ile Val Leu Ile
 195 200 205

Ala Val Val Gly Gly Ile Leu Tyr Gln Ser Ala Trp Ile Ile Glu Pro
 210 215 220

Lys Leu Trp Ile Ile Gly Thr Ile Phe Pro Ile Ala Gly Tyr Ser Leu
 225 230 235 240

Gly Phe Phe Leu Ala Arg Leu Ala Gly Gln Pro Trp Tyr Arg Cys Arg
 245 250 255

Thr Val Ala Leu Glu Thr Gly Met Gln Asn Thr Gln Leu Cys Ser Thr
 260 265 270

Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Asn Leu Val Phe Thr
 275 280 285

Phe Pro Leu Ile Tyr Thr Val Phe Gln Leu Val Phe Ala Ala Ile Ile
 290 295 300

Leu Gly Met Tyr Val Thr Tyr Lys Lys Cys His Gly Lys Asn Asp Ala
 305 310 315 320

Glu Phe Leu Glu Lys Thr Asp Asn Asp Met Asp Pro Met Pro Ser Phe
 325 330 335

Gln Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys
 340 345

<210> 43

<211> 348

<212> PRT

<213> Mus musculus

<400> 43

Met Asp Asn Ser Ser Val Cys Pro Pro Asn Ala Thr Val Cys Glu Gly
 1 5 10 15

Asp Ser Cys Val Val Pro Glu Ser Asn Phe Asn Ala Ile Leu Asn Thr
 20 25 30

Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Met Val Met Phe Ser
 35 40 45

Met Gly Cys Asn Val Glu Val His Lys Phe Leu Gly His Ile Lys Arg
 50 55 60

Pro Trp Gly Ile Phe Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro
 65 70 75 80

Leu Thr Gly Phe Ile Leu Ser Val Ala Ser Gly Ile Leu Pro Val Gln
 85 90 95

Ala Val Val Val Leu Ile Met Gly Cys Cys Pro Gly Gly Thr Gly Ser
 100 105 110

Asn Ile Leu Ala Tyr Trp Ile Asp Gly Asp Met Asp Leu Ser Val Ser
 115 120 125

Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu Cys
 130 135 140

Leu Phe Val Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val Ile
 145 150 155 160

Pro Tyr Asp Ser Ile Gly Ile Ser Leu Val Ala Leu Val Ile Pro Val
 165 170 175

Ser Phe Gly Met Phe Val Asn His Lys Trp Pro Gln Lys Ala Lys Ile
 180 185 190
 Ile Leu Lys Ile Gly Ser Ile Thr Gly Val Ile Leu Ile Val Leu Ile
 195 200 205
 Ala Val Ile Gly Gly Ile Leu Tyr Gln Ser Ala Trp Ile Ile Glu Pro
 210 215 220
 Lys Leu Trp Ile Ile Gly Thr Ile Phe Pro Ile Ala Gly Tyr Ser Leu
 225 230 235 240
 Gly Phe Phe Leu Ala Arg Leu Ala Gly Gln Pro Trp Tyr Arg Cys Arg
 245 250 255
 Thr Val Ala Leu Glu Thr Gly Met Gln Asn Thr Gln Leu Cys Ser Thr
 260 265 270
 Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Asn Leu Val Phe Thr
 275 280 285
 Phe Pro Leu Ile Tyr Thr Val Phe Gln Leu Val Phe Ala Ala Val Ile
 290 295 300
 Leu Gly Ile Tyr Val Thr Tyr Arg Lys Cys Tyr Gly Lys Asn Asp Ala
 305 310 315 320
 Glu Phe Leu Glu Lys Thr Asp Asn Glu Met Asp Ser Arg Pro Ser Phe
 325 330 335
 Asp Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys
 340 345

<210> 44
 <211> 348
 <212> PRT
 <213> Mus musculus

<400> 44
 Met Asp Asn Ser Ser Val Cys Pro Pro Asn Ala Thr Val Cys Glu Gly
 1 5 10 15
 Asp Ser Cys Val Val Pro Glu Ser Asn Phe Asn Ala Ile Leu Asn Thr
 20 25 30
 Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Met Val Met Phe Ser
 35 40 45
 Met Gly Cys Asn Val Glu Val His Lys Phe Leu Gly His Ile Lys Arg
 50 55 60
 Pro Trp Gly Ile Phe Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro
 65 70 75 80
 Leu Thr Gly Phe Ile Leu Ser Val Ala Ser Gly Ile Leu Pro Val Gln

Met Asp Asn Ser Ser Ile Cys Asn Pro Asn Ala Thr Ile Cys Glu Gly
 1 5 10 15
 Asp Ser Cys Ile Ala Pro Glu Ser Asn Phe Asn Ala Ile Leu Ser Val
 20 25 30
 Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Leu Val Met Phe Ser
 35 40 45
 Met Gly Cys Asn Val Glu Leu His Lys Phe Leu Gly His Leu Arg Arg
 50 55 60
 Pro Trp Gly Ile Val Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro
 65 70 75 80
 Leu Thr Gly Phe Val Leu Ser Val Ala Phe Gly Ile Leu Pro Val Gln
 85 90 95
 Ala Val Val Val Leu Ile Gln Gly Cys Cys Pro Gly Gly Thr Ala Ser
 100 105 110
 Asn Ile Leu Ala Tyr Trp Val Asp Gly Asp Met Asp Leu Ser Val Ser
 115 120 125
 Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu Cys
 130 135 140
 Leu Phe Ile Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val Ile
 145 150 155 160
 Pro Tyr Asp Ser Ile Gly Thr Ser Leu Val Ala Leu Val Ile Pro Val
 165 170 175
 Ser Ile Gly Met Tyr Val Asn His Lys Trp Pro Gln Lys Ala Lys Ile
 180 185 190
 Ile Leu Lys Ile Gly Ser Ile Ala Gly Ala Ile Leu Ile Val Leu Ile
 195 200 205
 Ala Val Val Gly Gly Ile Leu Tyr Gln Ser Ala Trp Thr Ile Glu Pro
 210 215 220
 Lys Leu Trp Ile Ile Gly Thr Ile Tyr Pro Ile Ala Gly Tyr Gly Leu
 225 230 235 240
 Gly Phe Phe Leu Ala Arg Ile Ala Gly Gln Pro Trp Tyr Arg Cys Arg
 245 250 255
 Thr Val Ala Leu Glu Thr Gly Leu Gln Asn Thr Gln Leu Cys Ser Thr
 260 265 270
 Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Asn Leu Val Phe Thr
 275 280 285
 Phe Pro Leu Ile Tyr Ser Ile Phe Gln Ile Ala Phe Ala Ala Ile Leu
 290 295 300

Leu Gly Ala Tyr Val Ala Tyr Lys Lys Cys His Gly Lys Asn Asn Thr
 305 310 315 320

Glu Leu Gln Glu Lys Thr Asp Asn Glu Met Glu Pro Arg Ser Ser Phe
 325 330 335

Gln Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys
 340 345

<210> 46
 <211> 272
 <212> PRT
 <213> Homo sapiens

<400> 46
 Met Ala Ala Lys Val Phe Glu Ser Ile Gly Lys Phe Gly Leu Ala Leu
 1 5 10 15

Ala Val Ala Gly Gly Val Val Asn Ser Ala Leu Tyr Asn Val Asp Ala
 20 25 30

Gly His Arg Ala Val Ile Phe Asp Arg Phe Arg Gly Val Gln Asp Ile
 35 40 45

Val Val Gly Glu Gly Thr His Phe Leu Ile Pro Trp Val Gln Lys Pro
 50 55 60

Ile Ile Phe Asp Cys Arg Ser Arg Pro Arg Asn Val Pro Val Ile Thr
 65 70 75 80

Gly Ser Lys Asp Leu Gln Asn Val Asn Ile Thr Leu Arg Ile Leu Phe
 85 90 95

Arg Pro Val Ala Ser Gln Leu Pro Arg Ile Phe Thr Ser Ile Gly Glu
 100 105 110

Asp Tyr Asp Glu Arg Val Leu Pro Ser Ile Thr Thr Glu Ile Leu Lys
 115 120 125

Ser Val Val Ala Arg Phe Asp Ala Gly Glu Leu Ile Thr Gln Arg Glu
 130 135 140

Leu Val Ser Arg Gln Val Ser Asp Asp Leu Thr Glu Arg Ala Ala Thr
 145 150 155 160

Phe Gly Leu Ile Leu Asp Asp Val Ser Leu Thr His Leu Thr Phe Gly
 165 170 175

Lys Glu Phe Thr Glu Ala Val Glu Ala Lys Gln Val Ala Gln Gln Glu
 180 185 190

Ala Glu Arg Ala Arg Phe Val Val Glu Lys Ala Glu Gln Gln Lys Lys
 195 200 205

Ala Ala Ile Ile Ser Ala Glu Gly Asp Ser Lys Ala Ala Glu Leu Ile
 210 215 220

Ala Asn Ser Leu Ala Thr Ala Gly Asp Gly Leu Ile Glu Leu Arg Lys
 225 230 235 240
 Leu Glu Ala Ala Glu Asp Ile Ala Tyr Gln Leu Ser Arg Ser Arg Asn
 245 250 255
 Ile Thr Tyr Leu Pro Ala Gly Gln Ser Val Leu Leu Gln Leu Pro Gln
 260 265 270

<210> 47
 <211> 272
 <212> PRT
 <213> Rattus norvegicus

<400> 47
 Met Ala Ala Lys Val Phe Glu Ser Ile Gly Lys Phe Gly Leu Ala Leu
 1 5 10 15
 Ala Val Ala Gly Gly Val Val Asn Ser Ala Leu Tyr Asn Val Asp Ala
 20 25 30
 Gly His Arg Ala Val Ile Phe Asp Arg Phe Arg Gly Val Gln Asp Ile
 35 40 45
 Val Val Gly Glu Gly Thr His Phe Leu Ile Pro Trp Val Gln Lys Pro
 50 55 60
 Ile Ile Phe Asp Cys Arg Ser Arg Pro Arg Asn Val Pro Val Ile Thr
 65 70 75 80
 Gly Ser Lys Asp Leu Gln Asn Val Asn Ile Thr Leu Arg Ile Leu Phe
 85 90 95
 Arg Pro Val Ala Ser Gln Leu Pro Arg Ile Tyr Thr Ser Ile Gly Glu
 100 105 110
 Asp Tyr Asp Glu Arg Val Leu Pro Ser Ile Thr Thr Glu Ile Leu Lys
 115 120 125
 Ser Val Val Ala Arg Phe Asp Ala Gly Glu Leu Ile Thr Gln Arg Glu
 130 135 140
 Leu Val Ser Arg Gln Val Ser Asp Asp Leu Thr Glu Arg Ala Ala Thr
 145 150 155 160
 Phe Gly Leu Ile Leu Asp Asp Val Ser Leu Thr His Leu Thr Phe Gly
 165 170 175
 Lys Glu Phe Thr Glu Ala Val Glu Ala Lys Gln Val Ala Gln Gln Glu
 180 185 190
 Ala Glu Arg Ala Arg Phe Val Val Glu Lys Ala Glu Gln Gln Lys Lys

195	200	205
Ala Ala Ile Ile Ser Ala Glu Gly Asp Ser Lys Ala Ala Glu Leu Ile		
210	215	220
Ala Asn Ser Leu Ala Thr Ala Gly Asp Gly Leu Ile Glu Leu Arg Lys		
225	230	235
Leu Glu Ala Ala Glu Asp Ile Ala Tyr Gln Leu Ser Arg Ser Arg Asn		
	245	250
Ile Thr Tyr Leu Pro Ala Gly Gln Ser Val Leu Leu Gln Leu Pro Gln		
	260	270

<210> 48
 <211> 1798
 <212> PRT
 <213> *Drosophila melanogaster*

<400> 48

Met Glu Met Arg Glu Val Leu Ser Arg Glu Gly Arg Glu Ala Lys Asn
1 5 10 15
Leu Leu Val Tyr Gln Phe Cys Asp Glu Thr Thr Ser Ser Gly Ala Thr
20 25 30
Ser Gly Phe Gly Ser Thr Gly Gly Asp Val Gly Gly Gly Ser Gly Gly
35 40 45
Asp Gly Pro Ala Val Gly Ser Gly Gly Val Leu Leu Asn Gly Asp Cys
50 55 60
Tyr Arg Lys Pro Pro Met Val Pro Pro Lys Ser Pro Asn Gly Thr Pro
65 70 75 80
Lys Asn Cys Gln Ser Pro Thr Ser Pro Arg Leu Lys Ser Ser Ala Ser
85 90 95
Val Gly Cys Gly Gly Gly Ser Ser Gly Gly Pro Arg Val Arg Ser Ala
100 105 110
Ser Thr Gly Arg Asp Lys Lys Ser Glu Leu Gln Ala Arg Tyr Trp Ala
115 120 125
Leu Leu Phe Gly Asn Leu Gln Arg Ala Ile Asn Glu Ile Tyr Gln Thr
130 135 140
Val Glu Cys Tyr Glu Asn Ile Ser Ser Cys Gln Glu Thr Ile Leu Val
145 150 155 160
Leu Glu Asn Tyr Val Arg Asp Phe Lys Ala Leu Cys Glu Trp Phe Lys
165 170 175

Val	Ser	Trp	Asp	Tyr	Glu	Ser	Arg	Pro	Leu	Gln	Gln	Arg	Pro	Gln	Ser	180	185	190	
Leu	Ala	Trp	Glu	Val	Arg	Lys	Ser	Asn	Pro	Thr	Pro	Arg	Val	Arg	Thr	195	200	205	
Arg	Ser	Leu	Cys	Ser	Pro	Asn	Asn	Ser	Gly	Lys	Ser	Ser	Pro	Ala	Leu	210	215	220	
Phe	Pro	Gly	Thr	Gln	Ser	Gly	Glu	Thr	Ser	Pro	Phe	Cys	Asp	Asn	Gly	225	230	235	240
Gln	Ile	Ser	Pro	Arg	Lys	Leu	Leu	Arg	Ala	Tyr	Asp	Gln	Val	Pro	Lys	245	250	255	
Gly	Ala	Met	Arg	Leu	Asn	Val	Arg	Glu	Leu	Phe	Ala	Ala	Ser	Lys	Arg	260	265	270	
Ala	Thr	Gln	Gly	Ser	Ser	Gln	Ser	Asp	Asn	Met	Glu	Gly	Pro	Leu	Asp	275	280	285	
Leu	Ser	Gly	Asp	Lys	Ser	Asn	Phe	Val	Leu	Arg	Ser	Thr	Gln	Tyr	Ala	290	295	300	
Gln	Thr	Asp	Leu	Glu	Asp	Pro	His	Leu	Thr	Leu	Ala	Asp	Val	Arg	Glu	305	310	315	320
Lys	Met	Arg	Met	Glu	Ala	Glu	Glu	Arg	Glu	Ala	Gln	Asn	Arg	Ile	Glu	325	330	335	
Asn	Glu	Ala	Leu	Glu	Glu	Val	Thr	Ile	Pro	Ile	Asp	Asn	Glu	Asp	Ala	340	345	350	
Thr	Glu	Ser	Leu	Asn	Lys	Gln	Glu	Pro	Ser	Ser	Leu	Glu	Leu	Pro	Ile	355	360	365	
His	Asn	Val	Ala	Asp	Leu	Ser	Lys	Glu	Pro	Glu	Leu	Met	Glu	Ala	Ala	370	375	380	
Ser	Glu	Ala	Thr	Ala	Leu	Glu	Met	Thr	Val	Ala	Ser	Leu	Glu	Ser	Met	385	390	395	400
Glu	Asn	Ala	Leu	Leu	Asn	Gln	Gln	Ala	Asn	Lys	Glu	Pro	Thr	Pro	Pro	405	410	415	
Ser	Thr	Val	Ile	Lys	Pro	Leu	Ala	Glu	Ile	Leu	Lys	Lys	Pro	Gln	Pro	420	425	430	
Leu	Asn	Pro	Leu	Ser	Gly	Asn	Asn	Val	Gln	Asn	Ser	Pro	Leu	Lys	Tyr	435	440	445	
Ser	Ser	Val	Leu	Asn	Arg	Pro	Ser	Lys	Lys	Met	Ile	Pro	Pro	Pro	Gly	450	455	460	
Gly	Val	Ala	Ala	Gln	Lys	Thr	Ile	Ser	Thr	Lys	Pro	Gly	Leu	Val	Lys	465	470	475	480

Pro Asn Leu Thr Thr Thr Val Asn Gly Leu Arg Ser Thr Lys Thr Ala
 485 490 495
 Thr Ala Pro Pro Ala Ile Lys Thr Thr Gly Arg Ser Gly Leu Gln Arg
 500 505 510
 His Pro Arg Pro Ser Ser Lys Thr Glu Cys Tyr Gly Pro Pro Asn Asn
 515 520 525
 Val Ala Ser Arg Leu Ser Ala Arg Ser Arg Thr Ile Asn Thr Leu Lys
 530 535 540
 Ala Glu Asn Gln His Ser Glu Pro Lys Gln Ile Gln Pro Pro Thr Asp
 545 550 555 560
 Ala Asp Asp Gly Trp Leu Thr Val Lys Asn Arg Arg Arg Thr Ser Met
 565 570 575
 His Trp Ala Asn Arg Phe Asn Gln Pro Thr Gly Tyr Ala Ser Leu Pro
 580 585 590
 Thr Leu Ala Leu Leu Asn Glu Gln Gln Lys Glu Gln Glu His Lys Glu
 595 600 605
 Lys Gln Lys Gly Glu Asp Asp Gly Lys Val Ile Val Lys Thr Ile Ser
 610 615 620
 Ala Lys Thr Lys Ala Pro Ile Glu Val Ala Lys Ala Lys Ala Lys Thr
 625 630 635 640
 Ser Ile Val Ile Thr Arg Pro Glu Ile Lys Asn Ala Lys Ala Lys Val
 645 650 655
 Asn Ser Phe Pro Val Gln Lys Ser Asn Thr Asn Gln Val Lys Lys Pro
 660 665 670
 Glu Lys Gln Glu Lys Ser Asp Thr Thr Ala Pro Ala Ala Ile Ala Ser
 675 680 685
 Ser Arg Leu Lys Met Thr Ser Leu His Lys Glu Tyr Met Arg Ser Glu
 690 695 700
 Lys Asn Ala Leu Arg Lys Leu Gln Gln Lys Glu Gln Gly Asn Gln Gln
 705 710 715 720
 His Asn Ser Ser Ser Ser Ser Ala Glu Thr Val Val Glu Ser Cys Asn
 725 730 735
 Glu Asp His Ser Lys Ile Asp Ile Lys Ile Gln Thr Asn Cys Glu Phe
 740 745 750
 Ser Lys Thr Ile Gly Glu Leu Tyr Glu Ser Ile Ala His Cys Lys Leu
 755 760 765
 Pro Ser Gly Ser Leu Lys Thr Asn Ala Ser Thr Leu Ser Ala Cys Asp
 770 775 780

Glu Asn Glu Glu Gln Asn Thr Asp Asp Asn Glu Glu Glu Arg Asn Glu
 785 790 795 800
 Arg Ile Leu Gly Glu Val Gln Glu Ser Leu Glu Arg Gln Ile Arg Glu
 805 810 815
 Leu Glu Gln Thr Glu Ile Asp Val Asp Thr Glu Thr Asp Glu Thr Asp
 820 825 830
 Cys Glu Val Gln Leu Glu Glu Gln Asp Asp Gly Val Asp Gly Leu Glu
 835 840 845
 Met Gly Ser Gly Asp Asp Ser Ala Val Phe Val Thr Met Ser Asp Asp
 850 855 860
 Glu Asn Ala Ser Leu Glu Leu Arg Tyr Gln Ala Leu Leu Ser Asp Met
 865 870 875 880
 Ser Trp Asn Glu Arg Ala Glu Ala Leu Ala Thr Leu Gln Ala Tyr Val
 885 890 895
 Ala Arg His Pro Gly Arg Ala Gln Glu Leu His Gln Lys Leu Ser Ser
 900 905 910
 Pro Ser Arg Arg Arg Ser Leu Gln Glu Thr Leu Lys Lys Tyr Gln Ala
 915 920 925
 Lys Gln Ala Arg Ala Gln Gln Lys Arg Asn Leu Leu Gln Gln Glu Lys
 930 935 940
 Ala Ala Lys Leu Gln Gln Leu Phe Ser Arg Val Glu Asp Val Lys Ala
 945 950 955 960
 Ala Lys Asn Gln Ile Ile Glu Asp Lys Arg Gln Lys Met Gln Gly Arg
 965 970 975
 Leu Gln Arg Ala Ala Glu Asn Arg Glu Gln Tyr Leu Lys Gln Ile Ile
 980 985 990
 Glu Lys Ala His Asp Glu Glu Lys Lys Leu Lys Glu Ile Asn Phe Ile
 995 1000 1005
 Lys Asn Ile Glu Ala Gln Asn Lys Arg Leu Asp Leu Leu Glu Ser Ser
 1010 1015 1020
 Lys Glu Thr Glu Gly Arg Leu Gln Asp Leu Glu Gln Glu Arg Gln Lys
 1025 1030 1035 1040
 Arg Val Glu Glu Lys Leu Ala Lys Glu Ala Ala Val Glu Arg Arg Arg
 1045 1050 1055
 Gln Ala Leu Glu Lys Glu Arg Leu Leu Lys Leu Glu Lys Met Asn Glu
 1060 1065 1070
 Thr Arg Leu Glu Lys Glu Gln Arg Ile Gly Lys Met Gln Glu Gln Lys
 1075 1080 1085

Glu Lys Gln Arg Gln Ala Leu Ala Arg Glu Lys Ala Arg Asp Arg Glu
 1090 1095 1100
 Glu Arg Leu Leu Ala Leu Gln Val Gln Gln Gln Gln Thr Thr Glu Glu
 1105 1110 1115 1120
 Leu Gln Arg Lys Ile Leu Gln Lys Gln Met Glu Ser Ala Arg Arg His
 1125 1130 1135
 Glu Glu Asn Ile Glu His Ile Arg Gln Arg Ala Leu Glu Leu Thr Ile
 1140 1145 1150
 Pro Thr Arg Gln Ala Asp Glu Gly Arg Gly Asp Gln Asp Val Ser Glu
 1155 1160 1165
 Asp Ile Leu Asn Gly Asn Ala Thr Ser Thr Thr Asn Glu Asp Cys Asp
 1170 1175 1180
 Leu Ser Ser Ser Leu Ser Glu Val Gly Gly Asn Asn Ala His Thr Arg
 1185 1190 1195 1200
 Ser Tyr Lys Lys Lys Met Lys Lys Leu Lys Gln Arg Met Asn Gln Cys
 1205 1210 1215
 Ala Ala Glu Tyr Leu Glu Ser Leu Glu Ala Leu Pro Ala His Ala Arg
 1220 1225 1230
 Arg Asp Ser Thr Val Pro Lys Leu Leu Asn Leu Val Val Lys Gly Gly
 1235 1240 1245
 Gly Ala Gln Gly Leu Asp Arg Asn Leu Gly Asn Leu Leu Arg Val Ile
 1250 1255 1260
 Pro Lys Ala Gln Thr Leu Asp Phe Leu Ala Phe Leu Cys Met Asp Gly
 1265 1270 1275 1280
 Leu Gly Ile Leu Ala Asn His Val Ile Ser Lys Gly Met Asp Glu Asn
 1285 1290 1295
 Ser Glu Ile Ser Arg Lys Ser Val Tyr Leu Ala Ala Gln Leu Tyr Arg
 1300 1305 1310
 Asn Ala Cys Ser Val Cys Pro Gln Ile Ala Arg His Ala Leu Leu Gly
 1315 1320 1325
 Asn Ser Ile Thr Val Leu Phe Asp Ala Ile Asn Lys Ser Phe Gln Val
 1330 1335 1340
 Ile Leu Lys Ser Asn Arg Cys Thr Lys Glu Thr Phe Ser Asn Phe Trp
 1345 1350 1355 1360
 Pro Pro Lys Met Leu His Asn Lys Ser Val Ala Arg Gln Ser Ser Arg
 1365 1370 1375
 Leu Glu Ala Leu Ser Leu Pro Glu Glu Lys Ser Pro Gln His Pro Val
 1380 1385 1390

Glu Leu Ser Thr Glu Leu Met Leu Ala Cys Thr Glu Ala Leu Ser Ser
 1395 1400 1405
 Ser Tyr Val Lys Lys Asn Thr His Pro Lys Val Pro Glu Arg Leu Pro
 1410 1415 1420
 Asp Met Ile Asn Asp Cys Arg Phe His Trp Gln Asp Val Asn Lys Glu
 1425 1430 1435 1440
 Asp Met Leu Ala Asp Glu Phe Arg Lys Tyr Lys Cys Tyr Glu Lys Asn
 1445 1450 1455
 Pro Val Ile Ala Leu Pro His Pro Ser Leu Ser Ala Ser Leu Cys Arg
 1460 1465 1470
 Ser Leu Ser Ala Thr Pro Leu Lys Ile Asn Leu His Gln Phe Leu Gly
 1475 1480 1485
 Ser Gly Ile Leu Ile Leu Arg Leu Asn His His Arg His Pro Ala Thr
 1490 1495 1500
 Gly Ala Ser Phe Ser Asp Ser Cys Cys Thr Cys Cys Pro Lys Leu Thr
 1505 1510 1515 1520
 Thr Glu Ala Ala Val Ala Ala Val Ala Ala His Gln His Gln His Gln
 1525 1530 1535
 Asn Gln Gln Gln Gln Pro Asp Tyr Ala Val Ile Thr Gly Leu Ile Glu
 1540 1545 1550
 Ile Leu Ser Arg Arg Ile Gln Lys Val Arg Glu Ser Ile Glu Ser Asn
 1555 1560 1565
 Lys Ser Val Met Leu Ser Leu Leu Thr Thr Leu Gly Phe Leu Ser Arg
 1570 1575 1580
 Phe Ile Asp Val Cys Gln Pro Gly Pro Ala Asp Pro Thr Arg Leu Leu
 1585 1590 1595 1600
 Ser Ala Ala Lys Ser Thr Glu Leu Phe Gly Thr Val Ser Met Leu Tyr
 1605 1610 1615
 Gly Cys Val Met Pro Met Gly Glu Cys Ile Pro Pro Arg Thr Thr Ala
 1620 1625 1630
 Leu Ala Ala Ser Thr Phe His Leu Tyr Val Ser Leu Ala Ser Leu Asp
 1635 1640 1645
 Val Asn Thr Phe Gln Glu Thr Leu Thr Val Glu Gly Pro Leu Ser Leu
 1650 1655 1660
 Lys Leu Leu Asp Val Met Thr Val Ile Leu Asn Cys Ser Leu Val Asn
 1665 1670 1675 1680
 Asp Gln Trp Thr Thr Asn Ser Glu Ser Cys Pro Met Leu Ile Asp Leu
 1685 1690 1695

Val Ala Ser Met Ala Phe Phe Cys Val Asn Asn Arg Arg His Gln Asp
1700 1705 1710

Leu Leu Ile Ser Glu Gln Tyr Ala Val Ile Phe Lys Arg Met Ala Lys
1715 1720 1725

Leu Pro Thr Gln Phe Asn Pro Val Ile Tyr Pro Phe Leu Val Thr Val
1730 1735 1740

Ser Phe Asn Asn Pro Pro Ala Arg Glu Phe Leu Ser Lys Asp Phe Asp
1745 1750 1755 1760

Leu Thr Phe Leu Asp Glu Tyr Ser Lys Ser Glu Met Ala Gln Arg Asn
1765 1770 1775

Val Val Ile Lys Leu Ile Asn Ser Arg Thr Lys Asp Lys Ile Ser Ala
1780 1785 1790

Gly Asn Lys Lys Asn Ala
1795

<210> 49
<211> 274
<212> PRT
<213> *Toxocara canis*

<400> 49
Met Ala Gly Ala Gln Lys Leu Leu Gly Arg Leu Gly Gln Ile Gly Val
1 5 10 15

Ala Leu Ala Val Thr Gly Gly Val Val Gln Ser Ala Leu Tyr Asn Val
20 25 30

Asp Gly Gly Gln Arg Ala Val Ile Phe Asp Arg Phe Thr Gly Val Lys
35 40 45

Pro Asp Val Val Gly Glu Gly Thr His Phe Leu Ile Pro Trp Val Gln
50 55 60

Arg Pro Ile Ile Phe Asp Ile Arg Ser Thr Pro Arg Ala Ile Ser Thr
65 70 75 80

Ile Thr Gly Ser Lys Asp Leu Gln Asn Val Ser Ile Thr Leu Arg Ile
85 90 95

Leu His Arg Pro Glu Pro Ser Lys Leu Pro Asn Ile Tyr Leu Asn Ile
100 105 110

Gly Gln Asp Tyr Ala Glu Arg Val Leu Pro Ser Ile Thr Asn Glu Val
115 120 125

Leu Lys Ala Val Val Ala Gln Phe Asp Ala His Glu Met Ile Thr Gln
130 135 140

Arg Glu Ser Val Ser His Arg Val Ser Val Glu Leu Ser Glu Arg Ala
145 150 155 160

Arg Gln Phe Gly Ile Leu Leu Asp Asp Ile Ala Ile Thr His Leu Ser
 165 170 175
 Phe Gly Arg Glu Phe Thr Glu Ala Val Glu Met Lys Gln Val Ala Gln
 180 185 190
 Gln Glu Ala Glu Lys Ala Arg Tyr Leu Val Glu Thr Ala Glu Gln Met
 195 200 205
 Lys Ile Ala Ala Ile Thr Thr Ala Glu Gly Asp Ala Gln Ala Ala Lys
 210 215 220
 Leu Leu Ala Gln Ala Phe Lys Asp Ala Gly Asp Gly Leu Ile Glu Leu
 225 230 235 240
 Arg Lys Ile Glu Ala Ala Glu Glu Ile Ala Glu Arg Met Ser Lys Thr
 245 250 255
 Arg Asn Val Ile Tyr Leu Pro Gly Asn Gln Asn Thr Leu Phe Asn Leu
 260 265 270
 Pro Ala

<210> 50
 <211> 402
 <212> PRT
 <213> Caenorhabditis elegans

<400> 50
 Met Glu Lys Tyr Lys Asn Glu Leu Glu Ile Phe Lys Arg Met Tyr Phe
 1 5 10 15
 Lys Asn Tyr Pro Thr Ser Ser Lys Asp Glu Glu Ala Ala Ala Val Ile
 20 25 30
 Gln Lys Gly Gly Glu Phe Ile Gln Glu Ile Leu Pro Thr Ile Ile Ser
 35 40 45
 Thr Ser Arg Ala Tyr Asp Thr Asn Gln Lys Ala Leu Leu Leu Ala Glu
 50 55 60
 Gly Gly Lys Met Tyr Asn Val Leu Glu Asp Tyr Asn Glu Thr Ala Glu
 65 70 75 80
 Lys Met Leu Ser Lys Ser Val Arg Met Asn Pro Lys Asn Ala Asp Ala
 85 90 95
 Trp His Glu Leu Gly Leu Cys Val Met Lys Arg Arg Asp Leu Glu Phe
 100 105 110
 Ala Gln Ser Cys Phe Lys Ile Ala Leu Gly Ile Ser Lys Thr Ala Pro
 115 120 125
 Ile Leu Thr Ser Leu Ala Val Ala Met Arg Leu Val Ala Leu Glu His

<213> Homo sapiens

<400> 51

Met	Gly	Trp	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Thr	Gln	Cys	Leu	Gly	Val	
1				5					10					15		
Pro	Gly	Gln	Arg	Ser	Pro	Leu	Asn	Asp	Phe	Gln	Val	Leu	Arg	Gly	Thr	
			20					25					30			
Glu	Leu	Gln	His	Leu	Leu	His	Ala	Val	Val	Pro	Gly	Pro	Trp	Gln	Glu	
		35					40					45				
Asp	Val	Ala	Asp	Ala	Glu	Glu	Cys	Ala	Gly	Arg	Cys	Gly	Pro	Leu	Met	
	50					55					60					
Asp	Cys	Arg	Ala	Phe	His	Tyr	Asn	Val	Ser	Ser	His	Gly	Cys	Gln	Leu	
65					70					75					80	
Leu	Pro	Trp	Thr	Gln	His	Ser	Pro	His	Thr	Arg	Leu	Arg	Arg	Ser	Gly	
				85					90					95		
Arg	Cys	Asp	Leu	Phe	Gln	Lys	Lys	Asp	Tyr	Val	Arg	Thr	Cys	Ile	Met	
		100						105					110			
Asn	Asn	Gly	Val	Gly	Tyr	Arg	Gly	Thr	Met	Ala	Thr	Thr	Val	Gly	Gly	
		115					120						125			
Leu	Pro	Cys	Gln	Ala	Trp	Ser	His	Lys	Phe	Pro	Asn	Asp	His	Lys	Tyr	
	130					135					140					
Thr	Pro	Thr	Leu	Arg	Asn	Gly	Leu	Glu	Glu	Asn	Phe	Cys	Arg	Asn	Pro	
145					150					155					160	
Asp	Gly	Asp	Pro	Gly	Gly	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	Ala	Val	
				165					170					175		
Arg	Phe	Gln	Ser	Cys	Gly	Ile	Lys	Ser	Cys	Arg	Glu	Ala	Ala	Cys	Val	
			180					185					190			
Trp	Cys	Asn	Gly	Glu	Glu	Tyr	Arg	Gly	Ala	Val	Asp	Arg	Thr	Glu	Ser	
		195					200					205				
Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Gln	His	Pro	
	210					215					220					
Phe	Glu	Pro	Gly	Lys	Phe	Leu	Asp	Gln	Gly	Leu	Asp	Asp	Asn	Tyr	Cys	
225					230					235					240	
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	
				245					250					255		
Gln	Ile	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Arg	Cys	Gly	Ser	Glu	Ala	
			260					265					270			
Gln	Pro	Arg	Gln	Glu	Ala	Thr	Thr	Val	Ser	Cys	Phe	Arg	Gly	Lys	Gly	
		275					280					285				

Glu Gly Tyr Arg Gly Thr Ala Asn Thr Thr Thr Ala Gly Val Pro Cys
 290 295 300
 Gln Arg Trp Asp Ala Gln Ile Pro His Gln His Arg Phe Thr Pro Glu
 305 310 315 320
 Lys Tyr Ala Cys Lys Asp Leu Arg Glu Asn Phe Cys Arg Asn Pro Asp
 325 330 335
 Gly Ser Glu Ala Pro Trp Cys Phe Thr Leu Arg Pro Gly Met Arg Ala
 340 345 350
 Ala Phe Cys Tyr Gln Ile Arg Arg Cys Thr Asp Asp Val Arg Pro Gln
 355 360 365
 Asp Cys Tyr His Gly Ala Gly Glu Gln Tyr Arg Gly Thr Val Ser Lys
 370 375 380
 Thr Arg Lys Gly Val Gln Cys Gln Arg Trp Ser Ala Glu Thr Pro His
 385 390 395 400
 Lys Pro Gln Phe Thr Phe Thr Ser Glu Pro His Ala Gln Leu Glu Glu
 405 410 415
 Asn Phe Cys Arg Asn Pro Asp Gly Asp Ser His Gly Pro Trp Cys Tyr
 420 425 430
 Thr Met Asp Pro Arg Thr Pro Phe Asp Tyr Cys Ala Leu Arg Arg Cys
 435 440 445
 Ala Asp Asp Gln Pro Pro Ser Ile Leu Asp Pro Pro Asp Gln Val Gln
 450 455 460
 Phe Glu Lys Cys Gly Lys Arg Val Asp Arg Leu Asp Gln Arg Arg Ser
 465 470 475 480
 Lys Leu Arg Val Val Gly Gly His Pro Gly Asn Ser Pro Trp Thr Val
 485 490 495
 Ser Leu Arg Asn Arg Gln Gly Gln His Phe Cys Gly Gly Ser Leu Val
 500 505 510
 Lys Glu Gln Trp Ile Leu Thr Ala Arg Gln Cys Phe Ser Ser Cys His
 515 520 525
 Met Pro Leu Thr Gly Tyr Glu Val Trp Leu Gly Thr Leu Phe Gln Asn
 530 535 540
 Pro Gln His Gly Glu Pro Ser Leu Gln Arg Val Pro Val Ala Lys Met
 545 550 555 560
 Val Cys Gly Pro Ser Gly Ser Gln Leu Val Leu Leu Lys Leu Glu Arg
 565 570 575
 Ser Val Thr Leu Asn Gln Arg Val Ala Leu Ile Cys Leu Pro Pro Glu
 580 585 590

Trp Tyr Val Val Pro Pro Gly Thr Lys Cys Glu Ile Ala Gly Trp Gly
 595 600 605
 Glu Thr Lys Gly Thr Gly Asn Asp Thr Val Leu Asn Val Ala Leu Leu
 610 615 620
 Asn Val Ile Ser Asn Gln Glu Cys Asn Ile Lys His Arg Gly Arg Val
 625 630 635 640
 Arg Glu Ser Glu Met Cys Thr Glu Gly Leu Leu Ala Pro Val Gly Ala
 645 650 655
 Cys Glu Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr His Asn Cys
 660 665 670
 Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys Ala Arg Ser
 675 680 685
 Arg Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val Asp Trp Ile
 690 695 700
 His Lys Val Met Arg Leu Gly
 705 710

<210> 52
 <211> 711
 <212> PRT
 <213> Homo sapiens

<400> 52
 Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Thr Gln Cys Leu Gly Val
 1 5 10 15
 Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr
 20 25 30
 Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu
 35 40 45
 Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met
 50 55 60
 Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu
 65 70 75 80
 Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly
 85 90 95
 Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met
 100 105 110
 Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly Gly
 115 120 125
 Leu Pro Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Lys Tyr
 130 135 140

Thr	Pro	Thr	Leu	Arg	Asn	Gly	Leu	Glu	Glu	Asn	Phe	Cys	Arg	Asn	Pro	145	150	155	160
Asp	Gly	Asp	Pro	Gly	Gly	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	Ala	Val	165	170		175
Arg	Phe	Gln	Ser	Cys	Gly	Ile	Lys	Ser	Cys	Arg	Glu	Ala	Ala	Cys	Val	180	185		190
Trp	Cys	Asn	Gly	Glu	Glu	Tyr	Arg	Gly	Ala	Val	Asp	Arg	Thr	Glu	Ser	195	200		205
Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Gln	His	Pro	210	215		220
Phe	Glu	Pro	Gly	Lys	Phe	Leu	Asp	Gln	Gly	Leu	Asp	Asp	Asn	Tyr	Cys	225	230	235	240
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	245	250		255
Gln	Ile	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Arg	Cys	Gly	Ser	Glu	Ala	260	265		270
Gln	Pro	Arg	Gln	Glu	Ala	Thr	Thr	Val	Ser	Cys	Phe	Arg	Gly	Lys	Gly	275	280		285
Glu	Gly	Tyr	Arg	Gly	Thr	Ala	Asn	Thr	Thr	Thr	Ala	Gly	Val	Pro	Cys	290	295	300	
Gln	Arg	Trp	Asp	Ala	Gln	Ile	Pro	His	Gln	His	Arg	Phe	Thr	Pro	Glu	305	310	315	320
Lys	Tyr	Ala	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp	325	330		335
Gly	Ser	Glu	Ala	Pro	Trp	Cys	Phe	Thr	Leu	Arg	Pro	Gly	Met	Arg	Ala	340	345		350
Ala	Phe	Cys	Tyr	Gln	Ile	Arg	Arg	Cys	Thr	Asp	Asp	Val	Arg	Pro	Gln	355	360		365
Asp	Cys	Tyr	His	Gly	Ala	Gly	Glu	Gln	Tyr	Arg	Gly	Thr	Val	Ser	Lys	370	375	380	
Thr	Arg	Lys	Gly	Val	Gln	Cys	Gln	Arg	Trp	Ser	Ala	Glu	Thr	Pro	His	385	390	395	400
Lys	Pro	Gln	Phe	Thr	Phe	Thr	Ser	Glu	Pro	His	Ala	Gln	Leu	Glu	Glu	405	410		415
Asn	Phe	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Ser	His	Gly	Pro	Trp	Cys	Tyr	420	425		430
Thr	Met	Asp	Pro	Arg	Thr	Pro	Phe	Asp	Tyr	Cys	Ala	Leu	Arg	Arg	Cys	435	440		445

Ala Asp Asp Gln Pro Pro Ser Ile Leu Asp Pro Pro Asp Gln Val Gln
 450 455 460
 Phe Glu Lys Cys Gly Lys Arg Val Asp Arg Leu Asp Gln Arg Arg Ser
 465 470 475 480
 Lys Leu Arg Val Val Gly Gly His Pro Gly Asn Ser Pro Trp Thr Val
 485 490 495
 Ser Leu Arg Asn Arg Gln Gly Gln His Phe Cys Gly Gly Ser Leu Val
 500 505 510
 Lys Glu Gln Trp Ile Leu Thr Ala Arg Gln Cys Phe Ser Ser Cys His
 515 520 525
 Met Pro Leu Thr Gly Tyr Glu Val Trp Leu Gly Thr Leu Phe Gln Asn
 530 535 540
 Pro Gln His Gly Glu Pro Ser Leu Gln Arg Val Pro Val Ala Lys Met
 545 550 555 560
 Val Cys Gly Pro Ser Gly Ser Gln Leu Val Leu Leu Lys Leu Glu Arg
 565 570 575
 Ser Val Thr Leu Asn Gln Arg Val Ala Leu Ile Cys Leu Pro Pro Glu
 580 585 590
 Trp Tyr Val Val Pro Pro Gly Thr Lys Cys Glu Ile Ala Gly Trp Gly
 595 600 605
 Glu Thr Lys Gly Thr Gly Asn Asp Thr Val Leu Asn Val Ala Phe Leu
 610 615 620
 Asn Val Ile Ser Asn Gln Glu Cys Asn Ile Lys His Arg Gly Arg Val
 625 630 635 640
 Arg Glu Ser Glu Met Cys Thr Glu Gly Leu Leu Ala Pro Val Gly Ala
 645 650 655
 Cys Glu Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr His Asn Cys
 660 665 670
 Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys Ala Arg Ser
 675 680 685
 Arg Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val Asp Trp Ile
 690 695 700
 His Lys Val Met Arg Leu Gly
 705 710

<210> 53
 <211> 711
 <212> PRT
 <213> Homo sapiens

<400> 53

Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Thr Gln Tyr Leu Gly Val
1 5 10 15

Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr
20 25 30

Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu
35 40 45

Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met
50 55 60

Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu
65 70 75 80

Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly
85 90 95

Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met
100 105 110

Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly Gly
115 120 125

Leu Pro Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Lys Tyr
130 135 140

Thr Pro Thr Leu Arg Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn Pro
145 150 155 160

Asp Gly Asp Pro Gly Gly Pro Trp Cys Tyr Thr Thr Asp Pro Ala Val
165 170 175

Arg Phe Gln Ser Cys Gly Ile Lys Ser Cys Arg Glu Ala Ala Cys Val
180 185 190

Trp Cys Asn Gly Glu Glu Tyr Arg Gly Ala Val Asp Arg Thr Glu Ser
195 200 205

Gly Arg Glu Cys Gln Arg Trp Asp Leu Gln His Pro His Gln His Pro
210 215 220

Phe Glu Pro Gly Lys Phe Leu Asp Gln Gly Leu Asp Asp Asn Tyr Cys
225 230 235 240

Arg Asn Pro Asp Gly Ser Glu Arg Pro Trp Cys Tyr Thr Thr Asp Pro
245 250 255

Gln Ile Glu Arg Glu Phe Cys Asp Leu Pro Arg Cys Gly Ser Glu Ala
260 265 270

Gln Pro Arg Gln Glu Ala Thr Thr Val Ser Cys Phe Arg Gly Lys Gly
275 280 285

Glu Gly Tyr Arg Gly Thr Ala Asn Thr Thr Thr Ala Gly Val Pro Cys

290	295	300
Gln Arg Trp Asp Ala	Gln Ile Pro His	Gln His Arg Phe Thr Pro Glu
305	310	315 320
Lys Tyr Ala Cys	Lys Asp Leu Arg Glu Asn Phe Cys Arg Asn Pro Asp	
	325	330 335
Gly Ser Glu Ala Pro Trp Cys Phe Thr Leu Arg Pro Gly Met Arg Ala		
	340	345 350
Ala Phe Cys Tyr Gln Ile Arg Arg Cys Thr Asp Asp Val Arg Pro Gln		
	355	360 365
Asp Cys Tyr His Gly Ala Gly Glu Gln Tyr Arg Gly Thr Val Ser Lys		
	370	375 380
Thr Arg Lys Gly Val Gln Cys Gln Arg Trp Ser Ala Glu Thr Pro His		
	385	390 395 400
Lys Pro Gln Phe Thr Phe Thr Ser Glu Pro His Ala Gln Leu Glu Glu		
	405	410 415
Asn Phe Cys Arg Asn Pro Asp Gly Asp Ser His Gly Pro Trp Cys Tyr		
	420	425 430
Thr Met Asp Pro Arg Thr Pro Phe Asp Tyr Cys Ala Leu Arg Arg Cys		
	435	440 445
Ala Asp Asp Gln Pro Pro Ser Ile Leu Asp Pro Pro Asp Gln Val Gln		
	450	455 460
Phe Glu Lys Cys Gly Lys Arg Val Asp Arg Leu Asp Gln Arg Arg Ser		
	465	470 475 480
Lys Leu Arg Val Val Gly Gly His Pro Gly Asn Ser Pro Trp Thr Val		
	485	490 495
Ser Leu Arg Asn Arg Gln Gly Gln His Phe Cys Gly Gly Ser Leu Val		
	500	505 510
Lys Glu Gln Trp Ile Leu Thr Ala Arg Gln Cys Phe Ser Ser Cys His		
	515	520 525
Met Pro Leu Thr Gly Tyr Glu Val Trp Leu Gly Thr Leu Phe Gln Asn		
	530	535 540
Pro Gln His Gly Glu Pro Ser Leu Gln Arg Val Pro Val Ala Lys Met		
	545	550 555 560
Val Cys Gly Pro Ser Gly Ser Gln Leu Val Leu Leu Lys Leu Glu Arg		
	565	570 575
Ser Val Thr Leu Asn Gln Arg Val Ala Leu Ile Cys Leu Pro Pro Glu		
	580	585 590
Trp Tyr Val Val Pro Pro Gly Thr Lys Cys Glu Ile Ala Gly Trp Gly		

595 600 605
 Glu Thr Lys Gly Thr Gly Asn Asp Thr Val Leu Asn Val Ala Leu Leu
 610 615 620
 Asn Val Ile Ser Asn Gln Glu Cys Asn Ile Lys His Arg Gly Arg Val
 625 630 635 640
 Arg Glu Ser Glu Met Cys Thr Glu Gly Leu Leu Ala Pro Val Gly Ala
 645 650 655
 Cys Glu Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr His Asn Cys
 660 665 670
 Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys Ala Arg Ser
 675 680 685
 Arg Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val Asp Trp Ile
 690 695 700
 His Lys Val Met Arg Leu Gly
 705 710

<210> 54
 <211> 529
 <212> PRT
 <213> Homo sapiens

<400> 54
 Met Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln
 1 5 10 15
 Leu Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg His Ser
 20 25 30
 Gly Arg Cys Asp Leu Phe Gln Glu Lys Asp Tyr Ile Arg Thr Cys Ile
 35 40 45
 Met Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly
 50 55 60
 Gly Leu Ser Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Gln
 65 70 75 80
 Tyr Met Pro Thr Leu Arg Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn
 85 90 95
 Pro Asp Gly Asp Pro Gly Gly Pro Trp Cys His Thr Thr Asp Pro Ala
 100 105 110
 Val Arg Phe Gln Ser Cys Gly Ile Lys Ser Cys Arg Val Ala Ala Cys
 115 120 125
 Val Trp Cys Asn Gly Glu Glu Tyr Arg Gly Ala Val Asp Arg Thr Glu
 130 135 140

Ser Gly Arg Glu Cys Gln Arg Trp Asp Leu Gln His Pro His Gln His
 145 150 155 160
 Pro Phe Glu Pro Gly Lys Phe Leu Asp Gln Gly Leu Asp Asp Asn Tyr
 165 170 175
 Cys Arg Asn Pro Asp Gly Ser Glu Arg Pro Trp Cys Tyr Thr Thr Asp
 180 185 190
 Pro Gln Ile Glu Arg Glu Phe Cys Asp Leu Pro Arg Cys Gly Ser Glu
 195 200 205
 Ala Gln Pro Arg Gln Glu Ala Thr Ser Val Ser Cys Phe Arg Gly Lys
 210 215 220
 Gly Glu Gly Tyr Arg Gly Thr Ala Asn Thr Thr Thr Ala Gly Val Pro
 225 230 235 240
 Cys Gln Arg Trp Asp Ala Gln Ile Pro His Gln His Arg Phe Thr Pro
 245 250 255
 Glu Lys Tyr Ala Cys Lys Asp Leu Arg Glu Asn Phe Cys Arg Asn Pro
 260 265 270
 Asp Gly Ser Glu Ala Pro Trp Cys Phe Thr Leu Arg Pro Gly Met Arg
 275 280 285
 Val Gly Phe Cys Tyr Gln Ile Arg Arg Cys Thr Asp Asp Val Arg Pro
 290 295 300
 Gln Asp Cys Tyr His Gly Ala Gly Glu Gln Tyr Arg Gly Thr Val Ser
 305 310 315 320
 Lys Thr Arg Lys Gly Val Gln Cys Gln Arg Gly Ser Ala Glu Thr Pro
 325 330 335
 His Lys Pro Gln Phe Thr Phe Thr Ser Glu Pro His Ala Gln Leu Glu
 340 345 350
 Glu Asn Phe Cys Gln Thr Gln Met Gly Ile Ala Met Gly Pro Gly Ala
 355 360 365
 Thr Arg Trp Thr Gln Gly Pro His Ser Thr Thr Val Pro Cys Asp Ala
 370 375 380
 Ala Leu Met Thr Ser Arg His Gln Ser Trp Thr Pro Gln Thr Arg Cys
 385 390 395 400
 Ser Leu Arg Ser Val Ala Arg Gly Trp Ile Gly Trp Ile Ser Val Val
 405 410 415
 Pro Ser Cys Ala Trp Leu Gly Ala Ile Arg Ala Thr His Pro Gly Gln
 420 425 430
 Ser Ala Cys Gly Ile Gly Gln Gly Gln His Phe Cys Gly Gly Ser Leu
 435 440 445

Val Lys Glu Gln Trp Ile Leu Thr Ala Arg Gln Cys Phe Ser Ser Cys
 450 455 460

His Met Pro Leu Thr Gly Tyr Glu Val Trp Leu Gly Thr Leu Phe Gln
 465 470 475 480

Asn Pro Gln His Gly Glu Pro Gly Leu Gln Arg Val Pro Val Ala Lys
 485 490 495

Met Leu Cys Gly Pro Ser Gly Ser Gln Leu Val Leu Leu Lys Leu Glu
 500 505 510

Arg Ser Val Thr Leu Asn Gln Arg Val Ala Leu Ile Cys Leu Pro Pro
 515 520 525

Glu

<210> 55

<211> 716

<212> PRT

<213> Mus musculus

<400> 55

Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Val Gln Cys Ser Arg Ala
 1 5 10 15

Leu Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Leu Phe Arg Gly Thr
 20 25 30

Glu Leu Arg Asn Leu Leu His Thr Ala Val Pro Gly Pro Trp Gln Glu
 35 40 45

Asp Val Ala Asp Ala Glu Glu Cys Ala Arg Arg Cys Gly Pro Leu Leu
 50 55 60

Asp Cys Arg Ala Phe His Tyr Asn Met Ser Ser His Gly Cys Gln Leu
 65 70 75 80

Leu Pro Trp Thr Gln His Ser Leu His Thr Gln Leu Tyr His Ser Ser
 85 90 95

Leu Cys His Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met
 100 105 110

Asp Asn Gly Val Ser Tyr Arg Gly Thr Val Ala Arg Thr Ala Gly Gly
 115 120 125

Leu Pro Cys Gln Ala Trp Ser Arg Arg Phe Pro Asn Asp His Lys Tyr
 130 135 140

Thr Pro Thr Pro Lys Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn Pro
 145 150 155 160

Asp Gly Asp Pro Arg Gly Pro Trp Cys Tyr Thr Thr Asn Arg Ser Val
 165 170 175

Arg	Phe	Gln	Ser	Cys	Gly	Ile	Lys	Thr	Cys	Arg	Glu	Ala	Val	Cys	Val	180	185	190	
Leu	Cys	Asn	Gly	Glu	Asp	Tyr	Arg	Gly	Glu	Val	Asp	Val	Thr	Glu	Ser	195	200	205	
Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Ser	His	Pro	210	215	220	
Phe	Gln	Pro	Glu	Lys	Phe	Leu	Asp	Lys	Asp	Leu	Lys	Asp	Asn	Tyr	Cys	225	230	235	240
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	245	250	255	
Asn	Val	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Ser	Cys	Gly	Pro	Asn	Leu	260	265	270	
Pro	Pro	Thr	Val	Lys	Gly	Ser	Lys	Ser	Gln	Arg	Arg	Asn	Lys	Gly	Lys	275	280	285	
Ala	Leu	Asn	Cys	Phe	Arg	Gly	Lys	Gly	Glu	Asp	Tyr	Arg	Gly	Thr	Thr	290	295	300	
Asn	Thr	Thr	Ser	Ala	Gly	Val	Pro	Cys	Gln	Arg	Trp	Asp	Ala	Gln	Ser	305	310	315	320
Pro	His	Gln	His	Arg	Phe	Val	Pro	Glu	Lys	Tyr	Ala	Cys	Lys	Asp	Leu	325	330	335	
Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp	Gly	Ser	Glu	Ala	Pro	Trp	Cys	340	345	350	
Phe	Thr	Ser	Arg	Pro	Gly	Leu	Arg	Met	Ala	Phe	Cys	His	Gln	Ile	Pro	355	360	365	
Arg	Cys	Thr	Glu	Glu	Leu	Val	Pro	Glu	Gly	Cys	Tyr	His	Gly	Ser	Gly	370	375	380	
Glu	Gln	Tyr	Arg	Gly	Ser	Val	Ser	Lys	Thr	Arg	Lys	Gly	Val	Gln	Cys	385	390	395	400
Gln	His	Trp	Ser	Ser	Glu	Thr	Pro	His	Lys	Pro	Gln	Phe	Thr	Pro	Thr	405	410	415	
Ser	Ala	Pro	Gln	Ala	Gly	Leu	Glu	Ala	Asn	Phe	Cys	Arg	Asn	Pro	Asp	420	425	430	
Gly	Asp	Ser	His	Gly	Pro	Trp	Cys	Tyr	Thr	Leu	Asp	Pro	Asp	Ile	Leu	435	440	445	
Phe	Asp	Tyr	Cys	Ala	Leu	Gln	Arg	Cys	Asp	Asp	Asp	Gln	Pro	Pro	Ser	450	455	460	
Ile	Leu	Asp	Pro	Pro	Asp	Gln	Val	Val	Phe	Glu	Lys	Cys	Gly	Lys	Arg	465	470	475	480

Val Asp Lys Ser Asn Lys Leu Arg Val Val Gly Gly His Pro Gly Asn
 485 490 495
 Ser Pro Trp Thr Val Ser Leu Arg Asn Arg Gln Gly Gln His Phe Cys
 500 505 510
 Gly Gly Ser Leu Val Lys Glu Gln Trp Val Leu Thr Ala Arg Gln Cys
 515 520 525
 Ile Trp Ser Cys His Glu Pro Leu Thr Gly Tyr Glu Val Trp Leu Gly
 530 535 540
 Thr Ile Asn Gln Asn Pro Gln Pro Gly Glu Ala Asn Leu Gln Arg Val
 545 550 555 560
 Pro Val Ala Lys Ala Val Cys Gly Pro Ala Gly Ser Gln Leu Val Leu
 565 570 575
 Leu Lys Leu Glu Arg Pro Val Ile Leu Asn His His Val Ala Leu Ile
 580 585 590
 Cys Leu Pro Pro Glu Gln Tyr Val Val Pro Pro Gly Thr Lys Cys Glu
 595 600 605
 Ile Ala Gly Trp Gly Glu Ser Ile Gly Thr Ser Asn Asn Thr Val Leu
 610 615 620
 His Val Ala Ser Met Asn Val Ile Ser Asn Gln Glu Cys Asn Thr Lys
 625 630 635 640
 Tyr Arg Gly His Ile Gln Glu Ser Glu Ile Cys Thr Gln Gly Leu Val
 645 650 655
 Val Pro Val Gly Ala Cys Glu Gly Asp Tyr Gly Gly Pro Leu Ala Cys
 660 665 670
 Tyr Thr His Asp Cys Trp Val Leu Gln Gly Leu Ile Ile Pro Asn Arg
 675 680 685
 Val Cys Ala Arg Pro Arg Trp Pro Ala Ile Phe Thr Arg Val Ser Val
 690 695 700
 Phe Val Asp Trp Ile Asn Lys Val Met Gln Leu Glu
 705 710 715

<210> 56
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 56
 Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Val Asp Ser
 1 5 10 15

Lys Gly Phe Asp Glu Tyr Met Lys Glu Leu Gly Val Gly Ile Ala Leu

20	25	30
Arg Lys Met Gly Ala Met Ala Lys Pro Asp Cys Ile Val Thr Cys Asp		
35	40	45
Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln		
50	55	60
Phe Ser Cys Pro Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly		
65	70	75
Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln		
85	90	95
His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Lys		
100	105	110
Asp Gly Lys Leu Val Val Glu Cys Val Met Asn His Val Ala Cys Thr		
115	120	125
Arg Ile Tyr Glu Lys Val Glu		
130	135	

<210> 57
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 57
Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Val Asp Ser
1 5 10 15
Lys Gly Phe Asp Glu Tyr Met Lys Glu Leu Gly Val Gly Ile Ala Leu
20 25 30
Arg Lys Met Gly Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp
35 40 45
Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln
50 55 60
Phe Ser Cys Thr Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly
65 70 75 80
Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln
85 90 95
His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Lys
100 105 110
Asp Gly Lys Leu Val Val Glu Cys Val Met Asn Asn Val Thr Cys Thr
115 120 125
Arg Ile Tyr Glu Lys Val Glu
130 135

<210> 58
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 58
 Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Val Asp Ser
 1 5 10 15
 Arg Gly Phe Asp Glu Tyr Val Lys Glu Leu Gly Val Gly Ile Ala Leu
 20 25 30
 Arg Lys Met Asp Thr Ile Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp
 35 40 45
 Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln
 50 55 60
 Phe Ser Cys Thr Leu Gly Glu Asn Phe Glu Glu Thr Thr Ala Asp Gly
 65 70 75 80
 Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln
 85 90 95
 His Gln Glu Trp Asp Gly Lys Glu Asn Thr Ile Arg Arg Lys Leu Lys
 100 105 110
 Asp Gly Lys Leu Val Val Asp Cys Val Met Asn Ser Val Thr Cys Thr
 115 120 125
 Arg Ile Tyr Glu Lys Val Glu
 130 135

<210> 59
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 59
 Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Leu Asp Ser
 1 5 10 15
 Lys Gly Phe Asp Glu Tyr Met Lys Glu Leu Gly Val Gly Ile Ala Leu
 20 25 30
 Gln Lys Met Gly Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp
 35 40 45
 Gly Arg Asn Leu Thr Thr Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln
 50 55 60
 Phe Ser Cys Thr Leu Gly Asp Glu Phe Glu Glu Thr Thr Ala Asp Gly
 65 70 75 80
 Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln

85

90

95

His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Lys
 100 105 110

Asp Gly Lys Leu Val Val Glu Cys Val Met Asn Asn Val Thr Cys Thr
 115 120 125

Arg Ile Tyr Glu Lys Val Glu
 130 135

<210> 60

<211> 135

<212> PRT

<213> Bos taurus

<400> 60

Met Ala Thr Val Gln Gln Leu Val Gly Arg Trp Arg Leu Val Glu Ser
 1 5 10 15

Lys Gly Phe Asp Glu Tyr Met Lys Glu Val Gly Val Gly Met Ala Leu
 20 25 30

Arg Lys Val Gly Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Ser Asp
 35 40 45

Gly Lys Asn Leu Ser Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln
 50 55 60

Phe Ser Cys Lys Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly
 65 70 75 80

Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln
 85 90 95

His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Glu
 100 105 110

Asp Gly Lys Leu Val Val Val Cys Val Met Asn Asn Val Thr Cys Thr
 115 120 125

Arg Val Tyr Glu Lys Val Glu
 130 135

<210> 61

<211> 266

<212> PRT

<213> Homo sapiens

<400> 61

Met Asn Trp Ala Phe Leu Gln Gly Leu Leu Ser Gly Val Asn Lys Tyr
 1 5 10 15

Ser Thr Val Leu Ser Arg Ile Trp Leu Ser Val Val Phe Ile Phe Arg
 20 25 30

Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Glu Gln
 35 40 45
 Lys Asp Phe Val Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys
 50 55 60
 Tyr Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
 65 70 75 80
 Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
 85 90 95
 Tyr Arg Glu Glu Arg Glu Arg Lys His His Leu Lys His Gly Pro Asn
 100 105 110
 Ala Pro Ser Leu Tyr Asp Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp
 115 120 125
 Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ala Gly
 130 135 140
 Phe Leu Tyr Ile Phe His Arg Leu Tyr Lys Asp Tyr Asp Met Pro Arg
 145 150 155 160
 Val Val Ala Cys Ser Val Glu Pro Cys Pro His Thr Val Asp Cys Tyr
 165 170 175
 Ile Ser Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Thr
 180 185 190
 Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Ser Glu Val Phe Tyr Leu
 195 200 205
 Val Gly Lys Arg Cys Met Glu Ile Phe Gly Pro Arg His Arg Arg Pro
 210 215 220
 Arg Cys Arg Glu Cys Leu Pro Asp Thr Cys Pro Pro Tyr Val Leu Ser
 225 230 235 240
 Gln Gly Gly His Pro Glu Asp Gly Asn Ser Val Leu Met Lys Ala Gly
 245 250 255
 Ser Ala Pro Val Asp Ala Gly Gly Tyr Pro
 260 265

<210> 62
 <211> 265
 <212> PRT
 <213> Rattus norvegicus

<400> 62
 Met Asn Trp Gly Phe Leu Gln Gly Ile Leu Ser Gly Val Asn Lys Tyr
 1 5 10 15
 Ser Thr Ala Leu Gly Arg Ile Trp Leu Ser Val Val Phe Ile Phe Arg

20					25					30									
Val	Leu	Val	Tyr	Val	Val	Ala	Ala	Glu	Glu	Val	Trp	Asp	Asp	Glu	Gln				
35					40					45									
Lys	Asp	Phe	Ile	Cys	Asn	Thr	Lys	Gln	Pro	Gly	Cys	Pro	Asn	Val	Cys				
50					55					60									
Tyr	Asp	Glu	Phe	Phe	Pro	Val	Ser	His	Val	Arg	Leu	Trp	Ala	Leu	Gln				
65					70					75					80				
Leu	Ile	Leu	Val	Thr	Cys	Pro	Ser	Leu	Leu	Val	Val	Met	His	Val	Ala				
85					90					95									
Tyr	Arg	Glu	Glu	Arg	Glu	Arg	Lys	His	Arg	Leu	Lys	His	Gly	Pro	Asp				
100					105					110									
Ala	Pro	Ala	Leu	Tyr	Ser	Asn	Leu	Ser	Lys	Lys	Arg	Gly	Gly	Leu	Trp				
115					120					125									
Trp	Thr	Tyr	Leu	Leu	Ser	Leu	Ile	Phe	Lys	Ala	Ala	Val	Asp	Ser	Gly				
130					135					140									
Phe	Leu	Tyr	Ile	Phe	His	Cys	Ile	Tyr	Lys	Asp	Tyr	Asp	Met	Pro	Arg				
145					150					155					160				
Val	Val	Ala	Cys	Ser	Val	Gln	Pro	Cys	Pro	His	Thr	Val	Asp	Cys	Tyr				
165					170					175									
Ile	Ser	Arg	Pro	Thr	Glu	Lys	Lys	Val	Phe	Thr	Tyr	Phe	Met	Val	Val				
180					185					190									
Thr	Ala	Ala	Ile	Cys	Ile	Leu	Leu	Asn	Leu	Ser	Glu	Val	Ala	Tyr	Leu				
195					200					205									
Val	Gly	Lys	Arg	Cys	Met	Glu	Val	Phe	Arg	Pro	Arg	Arg	Gln	Lys	Thr				
210					215					220									
Ser	Arg	Arg	His	Gln	Leu	Pro	Asp	Thr	Cys	Pro	Pro	Tyr	Val	Ile	Ser				
225					230					235					240				
Lys	Gly	His	Pro	Gln	Asp	Glu	Ser	Thr	Val	Leu	Thr	Lys	Ala	Gly	Met				
245					250					255									
Ala	Thr	Val	Asp	Ala	Gly	Val	Tyr	Pro											
260					265														

<210> 63
 <211> 266
 <212> PRT
 <213> Mus musculus

<400> 63
 Met Asn Trp Gly Phe Leu Gln Gly Ile Leu Ser Gly Val Asn Lys Tyr
 1 5 10 15

Ser Thr Ala Leu Gly Arg Ile Trp Leu Ser Val Val Phe Ile Phe Arg
 20 25 30
 Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Asp Gln
 35 40 45
 Lys Asp Phe Ile Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys
 50 55 60
 Tyr Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
 65 70 75 80
 Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
 85 90 95
 Tyr Arg Glu Glu Arg Glu Arg Lys His Arg Leu Lys His Gly Pro Asn
 100 105 110
 Ala Pro Ala Leu Tyr Ser Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp
 115 120 125
 Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ser Gly
 130 135 140
 Phe Leu Tyr Ile Phe His Cys Ile Tyr Lys Asp Tyr Asp Met Pro Arg
 145 150 155 160
 Val Val Ala Cys Ser Val Thr Pro Cys Pro His Thr Val Asp Cys Tyr
 165 170 175
 Ile Ala Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Val
 180 185 190
 Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Ser Glu Val Val Tyr Leu
 195 200 205
 Val Gly Lys Arg Cys Met Glu Val Phe Arg Pro Arg Arg Arg Lys Ala
 210 215 220
 Ser Arg Arg His Gln Leu Pro Asp Thr Cys Pro Pro Tyr Val Ile Ser
 225 230 235 240
 Lys Gly Gly His Pro Gln Asp Glu Ser Val Ile Leu Thr Lys Ala Gly
 245 250 255
 Met Ala Thr Val Asp Ala Gly Val Tyr Pro
 260 265

<210> 64

<211> 273

<212> PRT

<213> Homo sapiens

<400> 64

Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr
 1 5 10 15

Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg
 20 25 30
 Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp His
 35 40 45
 Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val Cys
 50 55 60
 Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
 65 70 75 80
 Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
 85 90 95
 Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu Asn
 100 105 110
 Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu Trp
 115 120 125
 Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile Ala
 130 135 140
 Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro Pro
 145 150 155 160
 Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys Phe
 165 170 175
 Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val Ala
 180 185 190
 Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu Ile Tyr Leu
 195 200 205
 Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys Ala Gln Ala
 210 215 220
 Met Cys Thr Gly His His Pro His Gly Thr Thr Ser Ser Cys Lys Gln
 225 230 235 240
 Asp Asp Leu Leu Ser Gly Asp Leu Ile Phe Leu Gly Ser Asp Ser His
 245 250 255
 Pro Pro Leu Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr Ile
 260 265 270

Leu

<210> 65
 <211> 273
 <212> PRT
 <213> Homo sapiens

<220>

<221> VARIANT

<222> (41)

<223> Wherein Xaa is any amino acid.

<400> 65

Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr
1 5 10 15

Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg
20 25 30

Val Leu Val Tyr Leu Val Thr Ala Xaa Arg Val Trp Ser Asp Asp His
35 40 45

Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val Cys
50 55 60

Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
65 70 75 80

Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
85 90 95

Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu Asn
100 105 110

Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu Trp
115 120 125

Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile Ala
130 135 140

Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro Pro
145 150 155 160

Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys Phe
165 170 175

Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val Ala
180 185 190

Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu Ile Tyr Leu
195 200 205

Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys Ala Gln Ala
210 215 220

Met Cys Thr Gly His His Pro His Gly Thr Thr Ser Ser Cys Lys Gln
225 230 235 240

Asp Asp Leu Leu Ser Gly Asp Leu Ile Phe Leu Gly Ser Asp Ser His
245 250 255

Pro Pro Leu Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr Ile
260 265 270

Leu

<210> 66
<211> 434
<212> PRT
<213> Homo sapiens

<400> 66

Ala Lys Gln Gln Leu Asn Leu Arg Thr His Met Ala Asp Glu Asn Lys
1 5 10 15

Asn Glu Tyr Ala Ala Gln Leu Gln Asn Phe Asn Gly Glu Gln His Lys
20 25 30

His Phe Tyr Val Val Ile Pro Gln Ile Tyr Lys Gln Leu Gln Glu Met
35 40 45

Asp Glu Arg Arg Thr Ile Lys Leu Ser Glu Cys Tyr Arg Gly Phe Ala
50 55 60

Asp Ser Glu Arg Lys Val Ile Pro Ile Ile Ser Lys Cys Leu Glu Gly
65 70 75 80

Met Ile Leu Ala Ala Lys Ser Val Asp Glu Arg Arg Asp Ser Gln Met
85 90 95

Val Val Asp Ser Phe Lys Ser Gly Phe Glu Pro Pro Gly Asp Phe Pro
100 105 110

Phe Glu Asp Tyr Ser Gln His Ile Tyr Arg Thr Ile Ser Asp Gly Thr
115 120 125

Ile Ser Ala Ser Lys Gln Glu Ser Gly Lys Met Asp Ala Lys Thr Thr
130 135 140

Val Gly Lys Ala Lys Gly Lys Leu Trp Leu Phe Gly Lys Lys Pro Lys
145 150 155 160

Pro Gln Ser Pro Pro Leu Thr Pro Thr Ser Leu Phe Thr Ser Ser Thr
165 170 175

Pro Asn Gly Ser Gln Phe Leu Thr Phe Ser Ile Glu Pro Val His Tyr
180 185 190

Cys Met Asn Glu Ile Lys Thr Gly Lys Pro Arg Ile Pro Ser Phe Arg
195 200 205

Ser Leu Lys Arg Gly Gly Pro Ala Leu Glu Asp Phe Ser His Leu Pro
210 215 220

Pro Glu Gln Arg Arg Lys Lys Leu Gln Gln Arg Ile Asp Glu Leu Asn
225 230 235 240

Arg Glu Leu Gln Lys Glu Ser Asp Gln Lys Asp Ala Leu Asn Lys Met

245										250										255													
Lys	Asp	Val	Tyr	Glu	Lys	Asn	Pro	Gln	Met	Gly	Asp	Pro	Gly	Ser	Leu																		
				260				265					270																				
Gln	Pro	Lys	Leu	Ala	Glu	Thr	Met	Asn	Asn	Ile	Asp	Arg	Leu	Arg	Met																		
		275					280					285																					
Glu	Ile	His	Lys	Asn	Glu	Ala	Trp	Leu	Ser	Glu	Val	Glu	Gly	Lys	Thr																		
	290					295					300																						
Gly	Gly	Arg	Gly	Asp	Arg	Arg	His	Ser	Ser	Asp	Ile	Asn	His	Leu	Val																		
305					310					315				320																			
Thr	Gln	Gly	Arg	Glu	Ser	Pro	Glu	Gly	Ser	Tyr	Thr	Asp	Asp	Ala	Asn																		
				325					330					335																			
Gln	Glu	Val	Arg	Gly	Pro	Pro	Gln	Gln	His	Gly	His	His	Asn	Glu	Phe																		
		340					345						350																				
Asp	Asp	Glu	Phe	Glu	Asp	Asp	Asp	Pro	Leu	Pro	Ala	Ile	Gly	His	Cys																		
	355					360						365																					
Lys	Ala	Ile	Tyr	Pro	Phe	Asp	Gly	His	Asn	Glu	Gly	Thr	Leu	Ala	Met																		
	370				375					380																							
Lys	Glu	Gly	Glu	Val	Leu	Tyr	Ile	Ile	Glu	Glu	Asp	Lys	Gly	Asp	Gly																		
385					390				395					400																			
Trp	Thr	Arg	Ala	Arg	Arg	Gln	Asn	Gly	Glu	Glu	Gly	Tyr	Val	Pro	Thr																		
			405					410					415																				
Ser	Tyr	Ile	Asp	Val	Thr	Leu	Glu	Lys	Asn	Ser	Lys	Gly	Ala	Val	Thr																		
		420					425						430																				

Tyr Ile

<210> 67
 <211> 330
 <212> PRT
 <213> Homo sapiens

<400> 67
 Met Asp Glu Arg Arg Thr Ile Lys Leu Ser Glu Cys Tyr Arg Gly Phe
 1 5 10 15
 Ala Asp Ser Glu Arg Lys Val Ile Pro Ile Ile Ser Lys Cys Leu Glu
 20 25 30
 Gly Met Ile Leu Ala Ala Lys Ser Val Asp Glu Arg Arg Asp Ser Gln
 35 40 45
 Met Val Val Asp Ser Phe Lys Ser Gly Phe Glu Pro Pro Gly Asp Phe
 50 55 60

Pro Phe Glu Asp Tyr Ser Gln His Ile Tyr Arg Thr Ile Ser Asp Gly
 65 70 75 80
 Thr Ile Ser Ala Ser Lys Gln Glu Ser Gly Lys Met Asp Ala Lys Thr
 85 90 95
 Thr Val Gly Lys Ala Lys Gly Lys Leu Trp Leu Phe Gly Lys Lys Pro
 100 105 110
 Lys Gly Pro Ala Leu Glu Asp Phe Ser His Leu Pro Pro Glu Gln Arg
 115 120 125
 Arg Lys Lys Leu Gln Gln Arg Ile Asp Glu Leu Asn Arg Glu Leu Gln
 130 135 140
 Lys Glu Ser Asp Gln Lys Asp Ala Leu Asn Lys Met Lys Asp Val Tyr
 145 150 155 160
 Glu Lys Asn Pro Gln Met Gly Asp Pro Gly Ser Leu Gln Pro Lys Leu
 165 170 175
 Ala Glu Thr Met Asn Asn Ile Asp Arg Leu Arg Met Glu Ile His Lys
 180 185 190
 Asn Glu Ala Trp Leu Ser Glu Val Glu Gly Lys Thr Gly Gly Arg Gly
 195 200 205
 Asp Arg Arg His Ser Ser Asp Ile Asn His Leu Val Thr Gln Gly Arg
 210 215 220
 Glu Ser Pro Glu Gly Ser Tyr Thr Asp Asp Ala Asn Gln Glu Val Arg
 225 230 235 240
 Gly Pro Pro Gln Gln His Gly His His Asn Glu Phe Asp Asp Glu Phe
 245 250 255
 Glu Asp Asp Asp Pro Leu Pro Ala Ile Gly His Cys Lys Ala Ile Tyr
 260 265 270
 Pro Phe Asp Gly His Asn Glu Gly Thr Leu Ala Met Lys Glu Gly Glu
 275 280 285
 Val Leu Tyr Ile Ile Glu Glu Asp Lys Gly Asp Gly Trp Thr Arg Ala
 290 295 300
 Arg Arg Gln Asn Gly Glu Glu Gly Tyr Val Pro Thr Ser Tyr Ile Asp
 305 310 315 320
 Val Thr Leu Glu Lys Asn Ser Lys Gly Ser
 325 330

<210> 68

<211> 592

<212> PRT

<213> Homo sapiens

<400> 68

Met Ser Trp Gly Thr Glu Leu Trp Asp Gln Phe Asp Asn Leu Glu Lys
1 5 10 15

His Thr Gln Trp Gly Ile Asp Ile Leu Glu Lys Tyr Ile Lys Phe Val
20 25 30

Lys Glu Arg Thr Glu Ile Glu Leu Ser Tyr Ala Lys Gln Leu Arg Asn
35 40 45

Leu Ser Lys Lys Tyr Gln Pro Lys Lys Asn Ser Lys Glu Glu Glu Glu
50 55 60

Tyr Lys Tyr Thr Ser Cys Lys Ala Phe Ile Ser Asn Leu Asn Glu Met
65 70 75 80

Asn Asp Tyr Ala Gly Gln His Glu Val Ile Ser Glu Asn Met Ala Ser
85 90 95

Gln Ile Ile Val Asp Leu Ala Arg Tyr Val Gln Glu Leu Lys Gln Glu
100 105 110

Arg Lys Ser Asn Phe His Asp Gly Arg Lys Ala Gln Gln His Ile Glu
115 120 125

Thr Cys Trp Lys Gln Leu Glu Ser Ser Lys Arg Arg Phe Glu Arg Asp
130 135 140

Cys Lys Glu Ala Asp Arg Ala Gln Gln Tyr Phe Glu Lys Met Asp Ala
145 150 155 160

Asp Ile Asn Val Thr Lys Ala Asp Val Glu Lys Ala Arg Gln Gln Ala
165 170 175

Gln Ile Arg His Gln Met Ala Glu Asp Ser Lys Ala Asp Tyr Ser Ser
180 185 190

Ile Leu Gln Lys Phe Asn His Glu Gln His Glu Tyr Tyr His Thr His
195 200 205

Ile Pro Asn Ile Phe Gln Lys Ile Gln Glu Met Glu Glu Arg Arg Ile
210 215 220

Val Arg Met Gly Glu Ser Met Lys Thr Tyr Ala Glu Val Asp Arg Gln
225 230 235 240

Val Ile Pro Ile Ile Gly Lys Cys Leu Asp Gly Ile Val Lys Ala Ala
245 250 255

Glu Ser Ile Asp Gln Lys Asn Asp Ser Gln Leu Val Ile Glu Ala Tyr
260 265 270

Lys Ser Gly Phe Glu Pro Pro Gly Asp Ile Glu Phe Glu Asp Tyr Thr
275 280 285

Gln Pro Met Lys Arg Thr Val Ser Asp Asn Ser Leu Ser Asn Ser Arg
290 295 300

Gly	Glu	Gly	Lys	Pro	Asp	Leu	Lys	Phe	Gly	Gly	Lys	Ser	Lys	Gly	Lys		305	310	315	320
Leu	Trp	Pro	Phe	Ile	Lys	Lys	Asn	Lys	Ser	Pro	Lys	Gln	Gln	Lys	Glu		325	330		335
Pro	Leu	Ser	His	Arg	Phe	Asn	Glu	Phe	Met	Thr	Ser	Lys	Pro	Lys	Ile		340	345		350
His	Cys	Phe	Arg	Ser	Leu	Lys	Arg	Gly	Leu	Ser	Leu	Lys	Leu	Gly	Ala		355	360		365
Thr	Pro	Glu	Asp	Phe	Ser	Asn	Leu	Pro	Pro	Glu	Gln	Arg	Arg	Lys	Lys		370	375		380
Leu	Gln	Gln	Lys	Val	Asp	Glu	Leu	Asn	Lys	Glu	Ile	Gln	Lys	Glu	Met		385	390		395
Asp	Gln	Arg	Asp	Ala	Ile	Thr	Lys	Met	Lys	Asp	Val	Tyr	Leu	Lys	Asn		405	410		415
Pro	Gln	Met	Gly	Asp	Pro	Ala	Ser	Leu	Asp	His	Lys	Leu	Ala	Glu	Val		420	425		430
Ser	Gln	Asn	Ile	Glu	Lys	Leu	Arg	Val	Glu	Thr	Gln	Lys	Phe	Glu	Ala		435	440		445
Trp	Leu	Ala	Glu	Val	Glu	Gly	Arg	Leu	Pro	Ala	Arg	Asn	Glu	Gln	Ala		450	455		460
Arg	Arg	Gln	Ser	Gly	Leu	Tyr	Asp	Ser	Gln	Asn	Pro	Pro	Thr	Val	Asn		465	470		475
Asn	Cys	Ala	Gln	Asp	Arg	Glu	Ser	Pro	Asp	Gly	Ser	Tyr	Thr	Glu	Glu		485	490		495
Gln	Ser	Gln	Glu	Ser	Glu	Met	Lys	Val	Leu	Ala	Thr	Asp	Phe	Asp	Asp		500	505		510
Glu	Phe	Asp	Asp	Glu	Glu	Pro	Leu	Pro	Ala	Ile	Gly	Thr	Cys	Lys	Ala		515	520		525
Leu	Tyr	Thr	Phe	Glu	Gly	Gln	Asn	Glu	Gly	Thr	Ile	Ser	Val	Val	Glu		530	535		540
Gly	Glu	Thr	Leu	Tyr	Val	Ile	Glu	Glu	Asp	Lys	Gly	Asp	Gly	Trp	Thr		545	550		555
Arg	Ile	Arg	Arg	Asn	Glu	Asp	Glu	Glu	Gly	Tyr	Val	Pro	Thr	Ser	Tyr		565	570		575
Val	Glu	Val	Cys	Leu	Asp	Lys	Asn	Ala	Lys	Gly	Ala	Lys	Thr	Tyr	Ile		580	585		590

<210> 69
 <211> 679
 <212> PRT
 <213> Homo sapiens

<400> 69

Leu Trp Asn Gly Gly Glu Glu Glu Pro Pro Arg Arg Pro Arg Ala Arg
 1 5 10 15

Ser Cys Glu Pro Glu Glu Ala Ala Arg Thr Pro Gly Phe Pro Pro Ser
 20 25 30

Arg Gly Ser Arg Gly Ala Lys Gly Ser Pro Gly Arg Gly Thr Arg Glu
 35 40 45

Pro Arg Pro Pro Arg Gly Ala Pro Leu Arg Val Pro Cys Thr Met Ser
 50 55 60

Trp Gly Thr Glu Leu Trp Asp Gln Phe Asp Asn Leu Glu Lys His Thr
 65 70 75 80

Gln Trp Gly Ile Asp Ile Leu Glu Lys Tyr Ile Lys Phe Val Lys Glu
 85 90 95

Arg Thr Glu Ile Glu Leu Ser Tyr Ala Lys Gln Leu Arg Asn Leu Ser
 100 105 110

Lys Lys Tyr Gln Pro Lys Lys Asn Ser Lys Glu Glu Glu Glu Tyr Lys
 115 120 125

Tyr Thr Ser Cys Lys Ala Phe Ile Ser Asn Leu Asn Glu Met Asn Asp
 130 135 140

Tyr Ala Gly Gln His Glu Val Ile Ser Glu Asn Met Ala Ser Gln Ile
 145 150 155 160

Ile Val Asp Leu Ala Arg Tyr Val Gln Glu Leu Lys Gln Glu Arg Lys
 165 170 175

Ser Asn Phe His Asp Gly Arg Lys Ala Gln Gln His Ile Glu Thr Cys
 180 185 190

Trp Lys Gln Leu Glu Ser Ser Lys Arg Arg Phe Glu Arg Asp Cys Lys
 195 200 205

Glu Ala Asp Arg Ala Gln Gln Tyr Phe Glu Lys Met Asp Ala Asp Ile
 210 215 220

Asn Val Thr Lys Ala Asp Val Glu Lys Ala Arg Gln Gln Ala Gln Ile
 225 230 235 240

Arg His Gln Met Ala Glu Asp Ser Lys Ala Asp Tyr Ser Ser Ile Leu
 245 250 255

Gln Lys Phe Asn His Glu Gln His Glu Tyr Tyr His Thr His Ile Pro

	260						265						270					
Asn	Ile	Phe	Gln	Lys	Ile	Gln	Glu	Met	Glu	Glu	Arg	Arg	Ile	Val	Arg			
		275					280					285						
Met	Gly	Glu	Ser	Met	Lys	Thr	Tyr	Ala	Glu	Val	Asp	Arg	Gln	Val	Ile			
	290					295					300							
Pro	Ile	Ile	Gly	Lys	Cys	Leu	Asp	Gly	Ile	Val	Lys	Ala	Ala	Glu	Ser			
305					310					315					320			
Ile	Asp	Gln	Lys	Asn	Asp	Ser	Gln	Leu	Val	Ile	Glu	Ala	Tyr	Lys	Ser			
				325					330					335				
Gly	Phe	Glu	Pro	Pro	Gly	Asp	Ile	Glu	Phe	Glu	Asp	Tyr	Thr	Gln	Pro			
			340					345					350					
Met	Lys	Arg	Thr	Val	Ser	Asp	Asn	Ser	Leu	Ser	Asn	Ser	Arg	Gly	Glu			
		355					360					365						
Gly	Lys	Pro	Asp	Leu	Lys	Phe	Gly	Gly	Lys	Ser	Lys	Gly	Lys	Leu	Trp			
	370					375					380							
Pro	Phe	Ile	Lys	Lys	Asn	Lys	Leu	Met	Ser	Leu	Leu	Thr	Ser	Pro	His			
385					390					395					400			
Gln	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Ser	Ala	Ser	Pro	Ser	Ala	Val	Pro			
				405					410					415				
Asn	Gly	Pro	Gln	Ser	Pro	Lys	Gln	Gln	Lys	Glu	Pro	Leu	Ser	His	Arg			
			420					425					430					
Phe	Asn	Glu	Phe	Met	Thr	Ser	Lys	Pro	Lys	Ile	His	Cys	Phe	Arg	Ser			
		435					440					445						
Leu	Lys	Arg	Gly	Leu	Ser	Leu	Lys	Leu	Gly	Ala	Thr	Pro	Glu	Asp	Phe			
	450					455					460							
Ser	Asn	Leu	Pro	Pro	Glu	Gln	Arg	Arg	Lys	Lys	Leu	Gln	Gln	Lys	Val			
465					470					475					480			
Asp	Glu	Leu	Asn	Lys	Glu	Ile	Gln	Lys	Glu	Met	Asp	Gln	Arg	Asp	Ala			
				485					490					495				
Ile	Thr	Lys	Met	Lys	Asp	Val	Tyr	Leu	Lys	Asn	Pro	Gln	Met	Gly	Asp			
			500					505					510					
Pro	Ala	Ser	Leu	Asp	His	Lys	Leu	Ala	Glu	Val	Ser	Gln	Asn	Ile	Glu			
		515					520					525						
Lys	Leu	Arg	Val	Glu	Thr	Gln	Lys	Phe	Glu	Ala	Trp	Leu	Ala	Glu	Val			
		530				535					540							
Glu	Gly	Arg	Leu	Pro	Ala	Arg	Ser	Glu	Gln	Ala	Arg	Arg	Gln	Ser	Gly			
545					550					555					560			
Leu	Tyr	Asp	Ser	Gln	Asn	Pro	Pro	Thr	Val	Asn	Asn	Cys	Ala	Gln	Asp			

	565		570		575
Arg Glu Ser	Pro Asp Gly Ser Tyr Thr Glu Glu Gln Ser Gln Glu Ser				
	580		585		590
Glu Met Lys Val Leu Ala Thr Asp Phe Asp Asp Glu Phe Asp Asp Glu					
	595		600		605
Glu Pro Leu Pro Ala Ile Gly Thr Cys Lys Ala Leu Tyr Thr Phe Glu					
	610		615		620
Gly Gln Asn Glu Gly Thr Ile Ser Val Val Glu Gly Glu Thr Leu Tyr					
	625		630		640
Val Ile Glu Glu Asp Lys Gly Asp Gly Trp Thr Arg Ile Arg Arg Asn					
	645		650		655
Glu Asp Glu Glu Gly Tyr Val Pro Thr Ser Tyr Val Glu Val Cys Leu					
	660		665		670
Asp Lys Asn Ala Lys Asp Ser					
	675				

<210> 70
 <211> 674
 <212> PRT
 <213> Homo sapiens

<400> 70
Glu Glu Glu Pro Pro Arg Arg Pro Arg Ala Arg Ser Cys Glu Pro Glu
1 5 10 15
Glu Ala Ala Arg Thr Pro Gly Phe Pro Pro Ser Arg Gly Ser Arg Gly
20 25 30
Ala Lys Gly Ser Pro Gly Arg Gly Thr Arg Glu Pro Arg Pro Pro Arg
35 40 45
Gly Ala Pro Leu Arg Val Pro Cys Thr Met Ser Trp Gly Thr Glu Leu
50 55 60
Trp Asp Gln Phe Asp Asn Leu Glu Lys His Thr Gln Trp Gly Ile Asp
65 70 75 80
Ile Leu Glu Lys Tyr Ile Lys Phe Val Lys Glu Arg Thr Glu Ile Glu
85 90 95
Leu Ser Tyr Ala Lys Gln Leu Arg Asn Leu Ser Lys Lys Tyr Gln Pro
100 105 110
Lys Lys Asn Ser Lys Glu Glu Glu Glu Tyr Lys Tyr Thr Ser Cys Lys
115 120 125
Ala Phe Ile Ser Asn Leu Asn Glu Met Asn Asp Tyr Ala Gly Gln His
130 135 140

Glu	Val	Ile	Ser	Glu	Asn	Met	Ala	Ser	Gln	Ile	Ile	Val	Asp	Leu	Ala	145	150	155	160
Arg	Tyr	Val	Gln	Glu	Leu	Lys	Gln	Glu	Arg	Lys	Ser	Asn	Phe	His	Asp	165	170		175
Gly	Arg	Lys	Ala	Gln	Gln	His	Ile	Glu	Thr	Cys	Trp	Lys	Gln	Leu	Glu	180	185		190
Ser	Ser	Lys	Arg	Arg	Phe	Glu	Arg	Asp	Cys	Lys	Glu	Ala	Asp	Arg	Ala	195	200		205
Gln	Gln	Tyr	Phe	Glu	Lys	Met	Asp	Ala	Asp	Ile	Asn	Val	Thr	Lys	Ala	210	215		220
Asp	Val	Glu	Lys	Ala	Arg	Gln	Gln	Ala	Gln	Ile	Arg	His	Gln	Met	Ala	225	230	235	240
Glu	Asp	Ser	Lys	Ala	Asp	Tyr	Ser	Ser	Ile	Leu	Gln	Lys	Phe	Asn	His	245	250		255
Glu	Gln	His	Glu	Tyr	Tyr	His	Thr	His	Ile	Pro	Asn	Ile	Phe	Gln	Lys	260	265		270
Ile	Gln	Glu	Met	Glu	Glu	Arg	Arg	Ile	Val	Arg	Met	Gly	Glu	Ser	Met	275	280		285
Lys	Thr	Tyr	Ala	Glu	Val	Asp	Arg	Gln	Val	Ile	Pro	Ile	Ile	Gly	Lys	290	295	300	
Cys	Leu	Asp	Gly	Ile	Val	Lys	Ala	Ala	Glu	Ser	Ile	Asp	Gln	Lys	Asn	305	310	315	320
Asp	Ser	Gln	Leu	Val	Ile	Glu	Ala	Tyr	Lys	Ser	Gly	Phe	Glu	Pro	Pro	325	330		335
Gly	Asp	Ile	Glu	Phe	Glu	Asp	Tyr	Thr	Gln	Pro	Met	Lys	Arg	Thr	Val	340	345		350
Ser	Asp	Asn	Ser	Leu	Ser	Asn	Ser	Arg	Gly	Glu	Gly	Lys	Pro	Asp	Leu	355	360		365
Lys	Phe	Gly	Gly	Lys	Ser	Lys	Gly	Lys	Leu	Trp	Pro	Phe	Ile	Lys	Lys	370	375	380	
Asn	Lys	Leu	Met	Ser	Leu	Leu	Thr	Ser	Pro	His	Gln	Pro	Pro	Pro	Pro	385	390	395	400
Pro	Pro	Ala	Ser	Ala	Ser	Pro	Ser	Ala	Val	Pro	Asn	Gly	Pro	Gln	Ser	405	410		415
Pro	Lys	Gln	Gln	Lys	Glu	Pro	Leu	Ser	His	Arg	Phe	Asn	Glu	Phe	Met	420	425		430
Thr	Ser	Lys	Pro	Lys	Ile	His	Cys	Phe	Arg	Ser	Leu	Lys	Arg	Gly	Leu	435	440		445

Ser Leu Lys Leu Gly Ala Thr Pro Glu Asp Phe Ser Asn Leu Pro Pro
 450 455 460

Glu Gln Arg Arg Lys Lys Leu Gln Gln Lys Val Asp Glu Leu Asn Lys
 465 470 475 480

Glu Ile Gln Lys Glu Met Asp Gln Arg Asp Ala Ile Thr Lys Met Lys
 485 490 495

Asp Val Tyr Leu Lys Asn Pro Gln Met Gly Asp Pro Ala Ser Leu Asp
 500 505 510

His Lys Leu Ala Glu Val Ser Gln Asn Ile Glu Lys Leu Arg Val Glu
 515 520 525

Thr Gln Lys Phe Glu Ala Trp Leu Ala Glu Val Glu Gly Arg Leu Pro
 530 535 540

Ala Arg Ser Glu Gln Ala Arg Arg Gln Ser Gly Leu Tyr Asp Ser Gln
 545 550 555 560

Asn Pro Pro Thr Val Asn Asn Cys Ala Gln Asp Arg Glu Ser Pro Asp
 565 570 575

Gly Ser Tyr Thr Glu Glu Gln Ser Gln Glu Ser Glu Met Lys Val Leu
 580 585 590

Ala Thr Asp Phe Asp Asp Glu Phe Asp Asp Glu Glu Pro Leu Pro Ala
 595 600 605

Ile Gly Thr Cys Lys Ala Leu Tyr Thr Phe Glu Gly Gln Asn Glu Gly
 610 615 620

Thr Ile Ser Val Val Glu Gly Glu Thr Leu Tyr Val Ile Glu Glu Asp
 625 630 635 640

Lys Gly Asp Gly Trp Thr Arg Ile Arg Arg Asn Glu Asp Glu Glu Gly
 645 650 655

Tyr Val Pro Thr Ser Tyr Val Glu Val Cys Leu Asp Lys Asn Ala Lys
 660 665 670

Asp Ser

<210> 71
 <211> 457
 <212> PRT
 <213> Homo sapiens

<400> 71
 Met Ser Leu Met Leu Asp Asp Gln Pro Pro Met Glu Ala Gln Tyr Ala
 1 5 10 15

Glu Glu Gly Pro Gly Pro Gly Ile Phe Arg Ala Glu Pro Gly Asp Gln
 20 25 30

Gln His Pro Ile Ser Gln Ala Val Cys Trp Arg Ser Met Arg Arg Gly
 35 40 45

Cys Ala Val Leu Gly Ala Leu Gly Leu Leu Ala Gly Ala Gly Val Gly
 50 55 60

Ser Trp Leu Leu Val Leu Tyr Leu Cys Pro Ala Ala Ser Gln Pro Ile
 65 70 75 80

Ser Gly Thr Leu Gln Asp Glu Glu Ile Thr Leu Ser Cys Ser Glu Ala
 85 90 95

Ser Ala Glu Glu Ala Leu Leu Pro Ala Leu Pro Lys Thr Val Ser Phe
 100 105 110

Arg Ile Asn Ser Glu Asp Phe Leu Leu Glu Ala Gln Val Arg Asp Gln
 115 120 125

Pro Arg Trp Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu Gly
 130 135 140

Leu Gln Ile Cys Trp Ser Leu Gly His Leu Arg Leu Thr His His Lys
 145 150 155 160

Gly Val Asn Leu Thr Asp Ile Lys Leu Asn Ser Ser Gln Glu Phe Ala
 165 170 175

Gln Leu Ser Pro Arg Leu Gly Gly Phe Leu Glu Glu Ala Trp Gln Pro
 180 185 190

Arg Asn Asn Cys Thr Ser Gly Gln Val Val Ser Leu Arg Cys Ser Glu
 195 200 205

Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ser Val
 210 215 220

Ala Pro Gly Arg Trp Pro Trp Gln Ala Ser Val Ala Leu Gly Phe Arg
 225 230 235 240

His Thr Cys Gly Gly Ser Val Leu Ala Pro Arg Trp Val Val Thr Ala
 245 250 255

Ala His Cys Met His Ser Phe Arg Leu Ala Arg Leu Ser Ser Trp Arg
 260 265 270

Val His Ala Gly Leu Val Ser His Ser Ala Val Arg Pro His Gln Gly
 275 280 285

Ala Leu Val Glu Arg Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn
 290 295 300

His Asp Tyr Asp Val Ala Leu Leu Arg Leu Gln Thr Ala Leu Asn Phe
 305 310 315 320

Ser Asp Thr Val Gly Ala Val Cys Leu Pro Ala Lys Glu Gln His Phe
 325 330 335

Pro Lys Gly Ser Arg Cys Trp Val Ser Gly Trp Gly His Thr His Pro
 340 345 350
 Ser His Thr Tyr Ser Ser Asp Met Leu Gln Asp Thr Val Val Pro Leu
 355 360 365
 Phe Ser Thr Gln Leu Cys Asn Ser Ser Cys Val Tyr Ser Gly Ala Leu
 370 375 380
 Thr Pro Arg Met Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala
 385 390 395 400
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Pro Asp Gly Asp Thr
 405 410 415
 Trp Arg Leu Val Gly Val Val Ser Trp Gly Arg Ala Cys Ala Glu Pro
 420 425 430
 Asn His Pro Gly Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp Ile
 435 440 445
 His Asp Thr Ala Gln Asp Ser Leu Leu
 450 455

<210> 72
 <211> 455
 <212> PRT
 <213> Mus musculus

<400> 72
 Met Ser Pro Thr Leu Asp Asp Gln Ser Pro Met Glu Ile Arg Cys Thr
 1 5 10 15
 Glu Glu Gly Ala Gly Pro Gly Ile Phe Arg Met Glu Leu Gly Asp Gln
 20 25 30
 Arg Gln Ser Ile Ser Gln Ser Gln Arg Trp Cys Cys Leu Gln Arg Gly
 35 40 45
 Cys Val Ile Leu Gly Val Leu Gly Leu Leu Ala Gly Ala Gly Ile Ala
 50 55 60
 Ser Trp Leu Leu Val Leu Tyr Leu Trp Pro Ala Ala Ser Pro Ser Ile
 65 70 75 80
 Ser Gly Thr Leu Gln Glu Glu Glu Met Thr Leu Asn Cys Pro Gly Val
 85 90 95
 Ser Cys Glu Glu Glu Leu Leu Pro Ser Leu Pro Lys Thr Val Ser Phe
 100 105 110
 Arg Ile Asn Gly Glu Asp Leu Leu Gln Val Gln Val Arg Ala Arg
 115 120 125
 Pro Asp Trp Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu Gly

130	135	140
Met His Ile Cys Lys Ser Leu Gly His Ile Arg Leu Thr Gln His Lys 145 150 155 160		
Ala Val Asn Leu Ser Asp Ile Lys Leu Asn Arg Ser Gln Glu Phe Ala 165 170 175		
Gln Leu Ser Ala Arg Pro Gly Gly Leu Val Glu Glu Ala Trp Lys Pro 180 185 190		
Ser Ala Asn Cys Pro Ser Gly Arg Ile Val Ser Leu Lys Cys Ser Glu 195 200 205		
Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ala Val 210 215 220		
Ala Ser Gly Arg Trp Pro Trp Gln Ala Ser Val Met Leu Gly Ser Arg 225 230 235 240		
His Thr Cys Gly Ala Ser Val Leu Ala Pro His Trp Val Val Thr Ala 245 250 255		
Ala His Cys Met Tyr Ser Phe Arg Leu Ser Arg Leu Ser Ser Trp Arg 260 265 270		
Val His Ala Gly Leu Val Ser His Gly Ala Val Arg Gln His Gln Gly 275 280 285		
Thr Met Val Glu Lys Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn 290 295 300		
His Asp Tyr Asp Val Ala Leu Leu Gln Leu Arg Thr Pro Ile Asn Phe 305 310 315 320		
Ser Asp Thr Val Asp Ala Val Cys Leu Pro Ala Lys Glu Gln Tyr Phe 325 330 335		
Pro Trp Gly Ser Gln Cys Trp Val Ser Gly Trp Gly His Thr Asp Pro 340 345 350		
Ser His Thr His Ser Ser Asp Thr Leu Gln Asp Thr Met Val Pro Leu 355 360 365		
Leu Ser Thr His Leu Cys Asn Ser Ser Cys Met Tyr Ser Gly Ala Leu 370 375 380		
Thr His Arg Met Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala 385 390 395 400		
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Pro Ser Gly Asp Thr 405 410 415		
Trp His Leu Val Gly Val Val Ser Trp Gly Arg Gly Cys Ala Glu Pro 420 425 430		
Asn Arg Pro Gly Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp Ile		

435	440	445
His Asp Thr Val Gln Val Arg		
450	455	
<210> 73		
<211> 445		
<212> PRT		
<213> Mus musculus		
<400> 73		
Met Glu Ile Arg Cys Thr Glu Glu Gly Ala Gly Pro Gly Ile Phe Arg		
1	5	10 15
Met Glu Leu Gly Asp Gln Arg Gln Ser Ile Ser Gln Ser Gln Arg Trp		
	20	25 30
Cys Cys Leu Gln Arg Gly Cys Val Ile Leu Gly Val Leu Gly Leu Leu		
	35	40 45
Ala Gly Ala Gly Ile Ala Ser Trp Leu Leu Val Leu Tyr Leu Trp Pro		
	50	55 60
Ala Ala Ser Pro Ser Ile Ser Gly Thr Leu Gln Glu Glu Glu Met Thr		
	65	70 75 80
Leu Asn Cys Pro Gly Val Ser Cys Glu Glu Glu Leu Leu Pro Ser Leu		
	85	90 95
Pro Lys Thr Val Ser Phe Arg Ile Asn Gly Glu Asp Leu Leu Leu Gln		
	100	105 110
Val Gln Val Arg Ala Arg Pro Asp Trp Leu Leu Val Cys His Glu Gly		
	115	120 125
Trp Ser Pro Ala Leu Gly Met His Ile Cys Lys Ser Leu Gly His Ile		
	130	135 140
Arg Leu Thr Gln His Lys Ala Val Asn Leu Ser Asp Ile Lys Leu Asn		
	145	150 155 160
Arg Ser Gln Glu Phe Ala Gln Leu Ser Ala Arg Pro Gly Gly Leu Val		
	165	170 175
Glu Glu Ala Trp Lys Pro Ser Ala Asn Cys Pro Ser Gly Arg Ile Val		
	180	185 190
Ser Leu Lys Cys Ser Glu Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile		
	195	200 205
Val Gly Gly Gln Ala Val Ala Ser Gly Arg Trp Pro Trp Gln Ala Ser		
	210	215 220
Val Met Leu Gly Ser Arg His Thr Cys Gly Ala Ser Val Leu Ala Pro		
	225	230 235 240

His Trp Val Val Thr Ala Ala His Cys Met Tyr Ser Phe Arg Leu Ser
 245 250 255
 Arg Leu Ser Ser Trp Arg Val His Ala Gly Leu Val Ser His Gly Ala
 260 265 270
 Val Arg Gln His Gln Gly Thr Met Val Glu Lys Ile Ile Pro His Pro
 275 280 285
 Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp Val Ala Leu Leu Gln Leu
 290 295 300
 Arg Thr Pro Ile Asn Phe Ser Asp Thr Val Gly Ala Val Cys Leu Pro
 305 310 315 320
 Ala Lys Glu Gln Tyr Phe Pro Trp Gly Ser Gln Cys Trp Val Ser Gly
 325 330 335
 Trp Gly His Thr Asp Pro Ser His Thr His Ser Ser Asp Thr Leu Gln
 340 345 350
 Asp Thr Met Val Pro Leu Leu Ser Thr His Leu Cys Asn Ser Ser Cys
 355 360 365
 Met Tyr Ser Gly Ala Leu Thr His Arg Met Leu Cys Ala Gly Tyr Leu
 370 375 380
 Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
 385 390 395 400
 Cys Pro Ser Gly Asp Thr Trp His Leu Val Gly Val Val Ser Trp Gly
 405 410 415
 Arg Gly Cys Ala Glu Pro Asn Arg Pro Gly Val Tyr Ala Lys Val Ala
 420 425 430
 Glu Phe Leu Asp Trp Ile His Asp Thr Val Gln Val Arg
 435 440 445

<210> 74

<211> 398

<212> PRT

<213> Homo sapiens

<400> 74

Met Ser Leu Met Leu Asp Asp Gln Pro Pro Met Glu Ala Gln Tyr Ala
 1 5 10 15
 Glu Glu Gly Pro Gly Pro Gly Ile Phe Arg Ala Glu Pro Gly Asp Gln
 20 25 30
 Gln His Pro Ile Ser Gln Ala Val Cys Trp Arg Ser Met Arg Arg Gly
 35 40 45
 Cys Ala Val Leu Gly Ala Leu Gly Leu Leu Ala Gly Ala Gly Val Gly
 50 55 60

Ser Trp Leu Leu Val Leu Tyr Leu Cys Pro Ala Ala Ser Gln Pro Ile
 65 70 75 80

Ser Gly Thr Leu Gln Asp Glu Glu Ile Thr Leu Ser Cys Ser Glu Ala
 85 90 95

Ser Ala Glu Glu Ala Leu Leu Pro Ala Leu Pro Lys Thr Val Ser Phe
 100 105 110

Arg Ile Asn Ser Glu Asp Phe Leu Leu Glu Ala Gln Val Arg Asp Gln
 115 120 125

Pro Arg Trp Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu Gly
 130 135 140

Leu Gln Ile Cys Trp Ser Leu Gly His Leu Arg Leu Thr His His Lys
 145 150 155 160

Gly Val Asn Leu Thr Asp Ile Lys Leu Asn Ser Ser Gln Glu Phe Ala
 165 170 175

Gln Leu Ser Pro Arg Leu Gly Gly Phe Leu Glu Glu Ala Trp Gln Pro
 180 185 190

Arg Asn Asn Cys Thr Ser Gly Gln Val Val Ser Leu Arg Cys Ser Glu
 195 200 205

Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ser Val
 210 215 220

Ala Pro Gly Arg Trp Pro Trp Gln Ala Ser Val Ala Leu Gly Phe Arg
 225 230 235 240

His Thr Cys Gly Gly Ser Val Leu Ala Pro Arg Trp Val Val Thr Ala
 245 250 255

Ala His Cys Met His Ser Phe Arg Leu Ala Arg Leu Ser Ser Trp Arg
 260 265 270

Val His Ala Gly Leu Val Ser His Ser Ala Val Arg Pro His Gln Gly
 275 280 285

Ala Leu Val Glu Arg Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn
 290 295 300

His Asp Tyr Asp Val Ala Leu Leu Arg Leu Gln Thr Ala Leu Asn Phe
 305 310 315 320

Ser Asp Thr Val Gly Ala Val Cys Leu Pro Ala Lys Glu Gln His Phe
 325 330 335

Pro Lys Gly Ser Arg Cys Trp Val Ser Gly Trp Gly His Thr His Pro
 340 345 350

Ser His Ser Leu Gln Leu Gly Tyr Ala Pro Gly His Gly Gly Ala Leu
 355 360 365

Val Gln His Ser Ala Leu Gln Gln Leu Leu Arg Val Gln Arg Ser Pro
 370 375 380

His Pro Pro His Ala Leu Arg Trp Leu Pro Gly Arg Lys Gly
 385 390 395

<210> 75
 <211> 311
 <212> PRT
 <213> Mus musculus

<400> 75
 Met His Ile Cys Lys Ser Leu Gly His Ile Arg Leu Thr Gln His Lys
 1 5 10 15

Ala Val Asn Leu Ser Asp Ile Lys Leu Asn Arg Ser Gln Glu Phe Ala
 20 25 30

Gln Leu Ser Ala Arg Pro Gly Gly Leu Val Glu Glu Ala Trp Lys Pro
 35 40 45

Ser Ala Asn Cys Pro Ser Gly Arg Ile Val Ser Leu Lys Cys Ser Glu
 50 55 60

Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ala Val
 65 70 75 80

Ala Ser Gly Arg Trp Pro Trp Gln Ala Ser Val Met Leu Gly Ser Arg
 85 90 95

His Thr Cys Gly Ala Ser Val Leu Ala Pro His Trp Val Val Thr Ala
 100 105 110

Ala His Cys Met Tyr Ser Phe Arg Leu Ser Arg Leu Ser Ser Trp Arg
 115 120 125

Val His Ala Gly Leu Val Ser His Gly Ala Val Arg Gln His Gln Gly
 130 135 140

Thr Met Val Glu Lys Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn
 145 150 155 160

His Asp Tyr Asp Val Ala Leu Leu Gln Leu Arg Thr Pro Ile Asn Phe
 165 170 175

Ser Asp Thr Val Asp Ala Val Cys Leu Pro Ala Lys Glu Gln Tyr Phe
 180 185 190

Pro Trp Gly Ser Gln Cys Trp Val Ser Gly Trp Gly His Thr Asp Pro
 195 200 205

Ser His Thr His Ser Ser Asp Thr Leu Gln Asp Thr Met Val Pro Leu
 210 215 220

Leu Ser Thr His Leu Cys Asn Ser Ser Cys Met Tyr Ser Gly Ala Leu

225 230 235 240
 Thr His Arg Met Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala
 245 250 255
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Pro Ser Gly Asp Thr
 260 265 270
 Trp His Leu Val Gly Val Val Ser Trp Gly Arg Gly Cys Ala Glu Pro
 275 280 285
 Asn Arg Pro Gly Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp Ile
 290 295 300
 His Asp Thr Val Gln Val Arg
 305 310

<210> 76
 <211> 199
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Reprolysin
 family zinc protease Consensus Sequence

<400> 76
 Lys Tyr Ile Glu Leu Phe Ile Val Val Asp His Gly Met Phe Thr Lys
 1 5 10 15
 Tyr Gly Ser Asp Leu Asn Lys Ile Arg Gln Arg Val His Gln Ile Val
 20 25 30
 Asn Leu Val Asn Glu Ile Tyr Arg Pro Leu Asn Ile Arg Val Val Leu
 35 40 45
 Val Gly Leu Glu Ile Trp Ser Asp Gly Asp Lys Ile Thr Val Gln Gly
 50 55 60
 Asp Ala Asn Asp Thr Leu His Arg Phe Leu Glu Trp Arg Glu Thr Asp
 65 70 75 80
 Leu Leu Lys Arg Lys Ser His Asp Asn Ala Gln Leu Leu Thr Gly Ile
 85 90 95
 Asp Phe Asp Gly Asn Thr Ile Gly Ala Ala Tyr Val Gly Gly Met Cys
 100 105 110
 Ser Pro Lys Arg Ser Val Gly Val Val Gln Asp His Ser Pro Ile Val
 115 120 125
 Leu Leu Val Ala Val Thr Met Ala His Glu Leu Gly His Asn Leu Gly
 130 135 140
 Met Thr His Asp Asp Ile Asn Lys Cys Thr Cys Glu Gly Gly Gly Gly
 145 150 155 160

Cys Ile Met Asn Pro Val Ala Ser Ser Ser Pro Gly Lys Lys Phe Ser
165 170 175

Asn Cys Ser Met Asp Asp Tyr Gln Gln Phe Leu Thr Lys Gly Lys Pro
180 185 190

Gln Cys Leu Leu Asn Lys Pro
195

<210> 77
<211> 51
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Thrombospondin
type 1 Consensus Sequence

<400> 77
Trp Gly Glu Trp Ser Glu Trp Ser Pro Cys Ser Val Thr Cys Gly Gly
1 5 10 15

Gly Val Gln Thr Arg Thr Arg Cys Cys Asn Pro Pro Pro Asn Gly Gly
20 25 30

Gly Pro Cys Thr Gly Pro Asp Thr Glu Thr Arg Ala Cys Asn Glu Gln
35 40 45

Pro Cys Pro
50

<210> 78
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Thrombospondin
type 1 domain Consensus Sequence

<400> 78
Ser Pro Trp Ser Glu Trp Ser Pro Cys Ser Val Thr Cys Gly Lys Gly
1 5 10 15

Ile Arg Thr Arg Gln Arg Thr Cys Asn Ser Pro Ala Gly Gly Lys Pro
20 25 30

Cys Thr Gly Asp Ala Gln Glu Thr Glu Ala Cys Met Met Asp Pro Cys
35 40 45

<210> 79
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Reprolysin
 family propeptide Consensus Sequence

<400> 79
 His Leu Glu Lys Asn Arg Ser Leu Leu Ala Pro Asp Phe Thr Val Thr
 1 5 10 15
 Thr Tyr Asp Asp Asp Gly Thr Leu Val Thr Glu His Pro Leu Ile Gln
 20 25 30
 Asp His Cys Tyr Tyr Gln Gly Tyr Val Glu Gly Tyr Pro Asn Ser Ala
 35 40 45
 Val Ser Leu Ser Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Leu Glu
 50 55 60
 Asn Leu Ser Tyr Gly Ile Glu Pro Leu Glu Ser Ser Asp Gly Phe Glu
 65 70 75 80
 His Ile Ile Tyr Gln Ile Glu His Leu Lys Thr Val Pro Gly Pro Cys
 85 90 95
 Gly Glu Cys Gly Ser Leu Ser Val Ser Thr Asp Ser Gln Tyr Gly Ile
 100 105 110
 Arg Ser Pro Ser Pro
 115

<210> 80
 <211> 751
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Alpha-2-macroglobulin family Consensus Sequence

<400> 80
 Ile Asp Glu Asp Asp Ile Thr Ile Arg Ser Tyr Phe Pro Glu Ser Trp
 1 5 10 15
 Leu Trp Glu Val Glu Glu Val Asp Arg Ser Pro Val Leu Thr Val Asn
 20 25 30
 Ile Thr Leu Pro Asp Ser Ile Thr Thr Trp Glu Ile Leu Ala Val Ser
 35 40 45
 Leu Ser Asn Thr Lys Gly Leu Cys Val Ala Asp Pro Val Glu Leu Thr
 50 55 60

Val Phe Gln Asp Phe Phe Leu Glu Leu Arg Leu Pro Tyr Ser Val Val
 65 70 75 80
 Arg Gly Glu Gln Val Glu Leu Arg Ala Val Leu Tyr Asn Tyr Leu Pro
 85 90 95
 Ser Gln Asp Ile Lys Val Val Val Gln Leu Glu Val Glu Pro Leu Cys
 100 105 110
 Gln Ala Gly Phe Cys Ser Leu Ala Thr Gln Arg Thr Arg Ser Ser Gln
 115 120 125
 Ser Val Arg Pro Lys Ser Leu Ser Ser Val Ser Phe Pro Val Val Val
 130 135 140
 Val Pro Leu Ala Ser Gly Leu Ser Leu Val Glu Val Val Ala Ser Val
 145 150 155 160
 Pro Glu Phe Phe Val Lys Asp Ala Val Val Lys Thr Leu Lys Val Glu
 165 170 175
 Pro Glu Gly Ala Arg Lys Glu Glu Thr Val Ser Ser Leu Leu Leu Pro
 180 185 190
 Pro Glu His Leu Gly Gly Gly Leu Glu Val Ser Glu Val Pro Ala Leu
 195 200 205
 Lys Leu Pro Asp Asp Val Pro Asp Thr Glu Ala Glu Ala Val Ile Ser
 210 215 220
 Val Gln Gly Asp Pro Val Ala Gln Ala Ile Gln Asn Thr Leu Ser Gly
 225 230 235 240
 Glu Gly Leu Asn Asn Leu Leu Arg Leu Pro Ser Gly Cys Gly Glu Gln
 245 250 255
 Asn Met Ile Tyr Met Ala Pro Thr Val Tyr Val Leu His Tyr Leu Asp
 260 265 270
 Glu Thr Trp Gln Trp Glu Lys Pro Gly Thr Lys Lys Lys Gln Lys Ala
 275 280 285
 Ile Asp Leu Ile Asn Lys Gly Tyr Gln Arg Gln Leu Asn Tyr Arg Lys
 290 295 300
 Ala Asp Gly Ser Tyr Ala Ala Phe Leu His Arg Ala Ser Ser Thr Trp
 305 310 315 320
 Leu Thr Ala Phe Val Leu Lys Val Phe Ser Gln Ala Arg Asn Tyr Val
 325 330 335
 Phe Ile Asp Glu Glu His Ile Cys Gly Ala Val Lys Trp Leu Ile Leu
 340 345 350
 Asn Gln Gln Lys Asp Asp Gly Val Phe Arg Glu Ser Gly Pro Val Ile
 355 360 365

His Asn Glu Met Lys Gly Gly Val Gly Asp Asp Ala Glu Val Glu Val
 370 375 380
 Thr Leu Thr Ala Phe Ile Thr Ile Ala Leu Leu Glu Ala Lys Leu Val
 385 390 395 400
 Cys Ile Ser Pro Val Val Ala Asn Ala Leu Ser Ile Leu Lys Ala Ser
 405 410 415
 Asp Tyr Leu Leu Glu Asn Tyr Ala Asn Gly Gln Arg Val Tyr Thr Leu
 420 425 430
 Ala Leu Thr Ala Tyr Ala Leu Ala Leu Ala Gly Val Leu His Lys Leu
 435 440 445
 Lys Glu Ile Leu Lys Ser Leu Lys Glu Glu Leu Tyr Lys Ala Leu Val
 450 455 460
 Lys Gly His Trp Glu Arg Pro Gln Lys Pro Lys Asp Ala Pro Gly His
 465 470 475 480
 Pro Tyr Ser Pro Gln Pro Gln Ala Ala Ala Val Glu Met Thr Ser Tyr
 485 490 495
 Ala Leu Leu Ala Leu Leu Thr Leu Leu Pro Phe Pro Lys Val Glu Met
 500 505 510
 Ala Pro Lys Val Val Lys Trp Leu Thr Glu Gln Gln Tyr Tyr Gly Gly
 515 520 525
 Gly Phe Gly Ser Thr Gln Asp Thr Val Met Ala Leu Gln Ala Leu Ser
 530 535 540
 Lys Tyr Gly Ile Ala Thr Pro Thr His Lys Glu Lys Asn Leu Ser Val
 545 550 555 560
 Thr Ile Gln Ser Pro Ser Gly Ser Phe Lys Ser His Phe Gln Ile Leu
 565 570 575
 Asn Asn Asn Ala Phe Leu Leu Arg Pro Val Glu Leu Pro Leu Asn Glu
 580 585 590
 Gly Phe Thr Val Thr Ala Lys Val Thr Gly Gln Gly Thr Leu Thr Leu
 595 600 605
 Val Thr Thr Tyr Arg Tyr Lys Val Leu Asp Lys Lys Asn Thr Phe Cys
 610 615 620
 Phe Asp Leu Lys Ile Glu Thr Val Pro Asp Thr Cys Val Glu Pro Lys
 625 630 635 640
 Gly Ala Lys Asn Ser Asp Tyr Leu Ser Ile Cys Thr Arg Tyr Ala Gly
 645 650 655
 Ser Arg Ser Asp Ser Gly Met Ala Ile Ala Asp Ile Ser Met Leu Thr
 660 665 670

Gly Phe Ile Pro Leu Lys Pro Asp Leu Lys Lys Leu Glu Asn Gly Val
675 680 685

Asp Arg Tyr Val Ser Lys Tyr Glu Ile Asp Gly Asn His Val Leu Leu
690 695 700

Tyr Leu Asp Lys Val Ser His Ser Glu Thr Glu Cys Val Gly Phe Lys
705 710 715 720

Ile His Gln Asp Phe Glu Val Gly Leu Leu Gln Pro Ala Ser Val Lys
725 730 735

Val Tyr Asp Tyr Tyr Glu Pro Asp Glu Gln Cys Thr Ala Phe Tyr
740 745 750

<210> 81

<211> 620

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Alpha-2-macroglobulin family N-terminal region

Consensus Sequence

<400> 81

Arg Leu Leu Trp Leu Leu Leu Leu Leu Leu Phe Phe Asp Ser Ser
1 5 10 15

Leu Gln Lys Pro Arg Tyr Met Val Ile Val Pro Ser Ile Leu Arg Thr
20 25 30

Glu Thr Pro Glu Lys Val Cys Val Gln Leu His Asp Leu Asn Glu Thr
35 40 45

Val Thr Val Thr Val Ser Leu His Ser Phe Pro Gly Lys Arg Asn Leu
50 55 60

Ser Ser Leu Phe Thr Val Leu Leu Ser Ser Lys Asp Leu Phe His Cys
65 70 75 80

Val Ser Phe Thr Val Pro Gln Pro Gly Leu Phe Lys Ser Ser Lys Gly
85 90 95

Glu Glu Ser Phe Val Val Val Gln Val Lys Gly Pro Thr His Thr Phe
100 105 110

Lys Glu Lys Val Thr Val Leu Val Ser Ser Arg Arg Gly Leu Val Phe
115 120 125

Ile Gln Thr Asp Lys Pro Ile Tyr Thr Pro Gly Gln Thr Val Arg Tyr
130 135 140

Arg Val Phe Ser Val Asp Glu Asn Leu Arg Pro Leu Asn Glu Leu Ile
145 150 155 160

Leu Val Tyr Ile Glu Asp Pro Glu Gly Asn Arg Val Asp Gln Trp Glu
 165 170 175
 Val Asn Lys Leu Glu Gly Gly Ile Phe Gln Leu Ser Phe Pro Ile Pro
 180 185 190
 Ser Glu Pro Ile Gln Gly Thr Trp Lys Ile Val Ala Arg Tyr Glu Ser
 195 200 205
 Gly Pro Glu Ser Asn Tyr Thr His Tyr Phe Glu Val Lys Glu Tyr Val
 210 215 220
 Leu Pro Ser Phe Glu Val Ser Ile Thr Pro Pro Lys Pro Phe Ile Tyr
 225 230 235 240
 Tyr Asp Asn Phe Lys Glu Phe Glu Val Thr Ile Cys Ala Arg Tyr Thr
 245 250 255
 Tyr Gly Lys Pro Val Pro Gly Val Ala Tyr Val Arg Phe Gly Val Lys
 260 265 270
 Asp Glu Asp Gly Lys Lys Glu Leu Leu Ala Gly Leu Glu Glu Arg Ala
 275 280 285
 Lys Leu Leu Asp Gly Asn Gly Glu Ile Cys Leu Ser Gln Glu Val Leu
 290 295 300
 Leu Lys Glu Leu Gln Leu Lys Asn Glu Asp Leu Glu Gly Lys Ser Leu
 305 310 315 320
 Tyr Val Ala Val Ala Val Ile Glu Ser Glu Gly Gly Asp Met Glu Glu
 325 330 335
 Ala Glu Leu Gly Gly Ile Lys Ile Val Arg Ser Pro Tyr Lys Leu Lys
 340 345 350
 Phe Val Lys Thr Pro Ser His Phe Lys Pro Gly Ile Pro Phe Phe Leu
 355 360 365
 Lys Val Leu Val Val Asp Pro Asp Gly Ser Pro Ala Pro Asn Val Pro
 370 375 380
 Val Lys Val Ser Ala Gln Asp Ala Ser Tyr Tyr Ser Asn Gly Thr Thr
 385 390 395 400
 Asp Glu Asp Gly Leu Ala Gln Phe Ser Ile Asn Thr Ser Gly Ile Ser
 405 410 415
 Ser Leu Ser Ile Thr Val Arg Thr Asn His Lys Glu Leu Pro Glu Glu
 420 425 430
 Val Gln Ala His Ala Glu Ala Gln Ala Thr Ala Tyr Ser Thr Val Ser
 435 440 445
 Leu Ser Lys Ser Tyr Ile His Leu Ser Ile Glu Arg Thr Leu Pro Cys
 450 455 460

Gly Pro Gly Val Gly Glu Gln Ala Asn Phe Ile Leu Arg Gly Lys Ser
 465 470 475 480
 Leu Gly Glu Leu Lys Ile Leu His Phe Tyr Tyr Leu Ile Met Ser Lys
 485 490 495
 Gly Lys Ile Val Lys Thr Gly Arg Glu Pro Arg Glu Pro Gly Gln Gly
 500 505 510
 Leu Phe Ser Leu Ser Ile Pro Val Thr Pro Asp Leu Ala Pro Ser Phe
 515 520 525
 Arg Leu Val Ala Tyr Tyr Ile Leu Pro Gln Gly Glu Val Val Ala Asp
 530 535 540
 Ser Val Trp Ile Asp Val Glu Asp Cys Cys Ala Asn Lys Leu Asp Leu
 545 550 555 560
 Ser Phe Ser Pro Ser Lys Asp Tyr Arg Leu Pro Ala Gln Gln Val Lys
 565 570 575
 Leu Arg Val Glu Ala Asp Pro Gln Ser Leu Val Ala Leu Arg Ala Val
 580 585 590
 Asp Gln Ala Val Tyr Leu Leu Lys Pro Lys Ala Lys Leu Ser Met Ser
 595 600 605
 Lys Val Tyr Asp Leu Leu Glu Lys Ser Asp Leu Gly
 610 615 620

<210> 82
 <211> 186
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Sodium Bile
 acid symporter family consensus sequence

<400> 82
 Ala Leu Gly Leu Phe Leu Met Met Phe Ser Met Gly Leu Lys Val Arg
 1 5 10 15
 Phe Glu Asp Leu Lys Glu Ala Leu Arg Arg Pro Lys Ala Leu Ile Leu
 20 25 30
 Gly Leu Leu Leu Gln Trp Ile Ile Met Pro Leu Leu Met Phe Ile Leu
 35 40 45
 Ala Trp Leu Leu Leu Arg Leu Pro Pro Glu Leu Ala Thr Gly Leu Ile
 50 55 60
 Leu Val Gly Cys Ala Pro Gly Gly Ala Met Ser Asn Val Trp Thr Tyr
 65 70 75 80
 Leu Ala Lys Gly Asp Val Glu Leu Ser Val Val Met Val Ala Leu Ser

	85	90	95
Thr Leu Leu Ala Pro Leu Val Thr Pro Leu Leu Ser Phe Leu Leu Ala	100	105	110
Gly Leu Leu Val His Val Asp Ala Val Ser Pro Trp Ser Leu Ile Lys	115	120	125
Ser Val Leu Val Tyr Val Ile Ile Pro Leu Ile Ala Gly Met Leu Thr	130	135	140
Arg Tyr Phe Leu Pro Glu Trp Phe Glu Gln Arg Val Leu Pro Val Leu	145	150	155
Ser Pro Ile Ser Leu Ile Gly Leu Leu Leu Thr Ile Val Val Ile Phe	165	170	175
Ala Leu Asn Gly Glu Val Ile Ala Ser Leu	180	185	

<210> 83
 <211> 191
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: SPFH
 domain/Band 7 family Consensus Sequence

<400> 83
 Val Ala Leu Leu Ile Ile Ile Ala Leu Val Val Ile Ala Met Ser Val
 1 5 10 15
 Lys Ile Val Lys Glu Tyr Glu Arg Gly Val Ile Phe Arg Leu Gly Arg
 20 25 30
 Tyr Val Arg Gln Val Val Gly Pro Gly Leu His Phe Ile Ile Pro Phe
 35 40 45
 Ile Asp Thr Val Lys Lys Val Asp Leu Arg Thr Val Val Tyr Asp Val
 50 55 60
 Pro Ser Gln Glu Ile Ile Thr Lys Asp Asn Val Val Val Ile Val Asp
 65 70 75 80
 Ala Val Val Tyr Tyr Arg Val Val Asp Pro Leu Lys Ala Val Tyr Glu
 85 90 95
 Val Glu Asp Ala Glu Arg Ala Leu Pro Gln Leu Ala Gln Thr Thr Leu
 100 105 110
 Arg Asn Val Ile Gly Gln Phe Thr Leu Asp Glu Ile Leu Thr Glu Arg
 115 120 125
 Glu Arg Ile Asn Ser Gln Leu Arg Glu Ile Leu Asp Glu Ala Thr Asp
 130 135 140

Pro Trp Gly Ile Lys Val Glu Arg Val Glu Ile Lys Asp Ile Arg Leu
 145 150 155 160

Pro Glu Glu Val Gln Arg Ala Met Ala Ala Gln Met Glu Ala Glu Arg
 165 170 175

Glu Ala Arg Ala Lys Ile Leu Glu Ala Glu Gly Glu Gln Glu Ala
 180 185 190

<210> 84

<211> 160

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Prohibitin
 homologues Consensus Sequence

<400> 84

Ala Ala Phe Tyr Val Ile Gly Glu Gly Glu Arg Gly Val Val Glu Arg
 1 5 10 15

Leu Gly Arg Val Leu Lys Val Leu Gly Pro Gly Leu His Phe Val Ile
 20 25 30

Pro Phe Ile Asp Asp Val Lys Arg Val Asp Leu Arg Ala Gln Thr Asp
 35 40 45

Asp Val Pro Pro Gln Glu Val Ile Thr Lys Asp Asn Val Thr Val Ser
 50 55 60

Val Asp Ala Val Val Tyr Tyr Arg Val Leu Asp Pro Leu Lys Ala Val
 65 70 75 80

Tyr Gly Val Leu Asp Ala Asp Tyr Arg Ala Leu Arg Gln Leu Ala Gln
 85 90 95

Thr Thr Leu Arg Ser Val Ile Gly Lys Arg Thr Leu Asp Glu Leu Leu
 100 105 110

Thr Asp Glu Arg Glu Lys Ile Ser Glu Asn Ile Arg Glu Glu Leu Asn
 115 120 125

Glu Ala Ala Glu Pro Trp Gly Ile Glu Val Glu Asp Val Glu Ile Lys
 130 135 140

Asp Ile Arg Leu Pro Glu Glu Ile Lys Glu Ala Met Glu Ala Gln Gln
 145 150 155 160

<210> 85

<211> 79

<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Kringle domain
Consensus Sequence

<400> 85

Cys Tyr His Gly Asn Gly Glu Asn Tyr Arg Gly Thr Ala Ser Thr Thr
1 5 10 15

Glu Ser Gly Ala Pro Cys Gln Arg Trp Asp Ser Gln Thr Pro His Arg
20 25 30

His Ser Lys Tyr Thr Pro Glu Arg Tyr Pro Ala Lys Gly Leu Gly Glu
35 40 45

Asn Tyr Cys Arg Asn Pro Asp Gly Asp Glu Arg Pro Trp Cys Tyr Thr
50 55 60

Thr Asp Pro Arg Val Arg Trp Glu Tyr Cys Asp Ile Pro Arg Cys
65 70 75

<210> 86

<211> 83

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Kringle domain
Consensus Sequence

<400> 86

Arg Asp Cys Tyr Ala Gly Asn Gly Glu Ser Tyr Arg Gly Thr Ala Ser
1 5 10 15

Thr Thr Lys Ser Gly Lys Pro Cys Gln Arg Trp Asp Ser Gln Thr Pro
20 25 30

His Leu His Arg Phe Thr Pro Glu Arg Phe Pro Glu Leu Gly Leu Glu
35 40 45

His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ser Glu Gly Pro Trp Cys
50 55 60

Tyr Thr Thr Asp Pro Asn Val Arg Trp Glu Tyr Cys Asp Ile Pro Gln
65 70 75 80

Cys Glu Ser

<210> 87

<211> 230

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Trypsin-like
serine protease Consensus Sequence

<400> 87

Arg Ile Val Gly Gly Ser Glu Ala Asn Ile Gly Ser Phe Pro Trp Gln
1 5 10 15

Val Ser Leu Gln Tyr Arg Gly Gly Arg His Phe Cys Gly Gly Ser Leu
20 25 30

Ile Ser Pro Arg Trp Val Leu Thr Ala Ala His Cys Val Tyr Gly Ser
35 40 45

Ala Pro Ser Ser Ile Arg Val Arg Leu Gly Ser His Asp Leu Ser Ser
50 55 60

Gly Glu Glu Thr Gln Thr Val Lys Val Ser Lys Val Ile Val His Pro
65 70 75 80

Asn Tyr Asn Pro Ser Thr Tyr Asp Asn Asp Ile Ala Leu Leu Lys Leu
85 90 95

Ser Glu Pro Val Thr Leu Ser Asp Thr Val Arg Pro Ile Cys Leu Pro
100 105 110

Ser Ser Gly Tyr Asn Val Pro Ala Gly Thr Thr Cys Thr Val Ser Gly
115 120 125

Trp Gly Arg Thr Ser Glu Ser Ser Gly Ser Leu Pro Asp Thr Leu Gln
130 135 140

Glu Val Asn Val Pro Ile Val Ser Asn Ala Thr Cys Arg Arg Ala Tyr
145 150 155 160

Ser Gly Gly Pro Ala Ile Thr Asp Asn Met Leu Cys Ala Gly Gly Leu
165 170 175

Glu Gly Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
180 185 190

Cys Asn Asp Pro Arg Trp Val Leu Val Gly Ile Val Ser Trp Gly Ser
195 200 205

Tyr Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Thr Arg Val Ser
210 215 220

Ser Tyr Leu Asp Trp Ile
225 230

<210> 88

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Trypsin
Consensus Sequence

<400> 88

Ile Val Gly Gly Arg Glu Ala Gln Ala Gly Ser Phe Pro Trp Gln Val
1 5 10 15

Ser Leu Gln Val Ser Ser Gly His Phe Cys Gly Gly Ser Leu Ile Ser
20 25 30

Glu Asn Trp Val Leu Thr Ala Ala His Cys Val Ser Gly Ala Ser Ser
35 40 45

Val Arg Val Val Leu Gly Glu His Asn Leu Gly Thr Thr Glu Gly Thr
50 55 60

Glu Gln Lys Phe Asp Val Lys Lys Ile Ile Val His Pro Asn Tyr Asn
65 70 75 80

Pro Asp Thr Asn Asp Ile Ala Leu Leu Lys Leu Lys Ser Pro Val Thr
85 90 95

Leu Gly Asp Thr Val Arg Pro Ile Cys Leu Pro Ser Ala Ser Ser Asp
100 105 110

Leu Pro Val Gly Thr Thr Cys Ser Val Ser Gly Trp Gly Arg Thr Lys
115 120 125

Asn Leu Gly Thr Ser Asp Thr Leu Gln Glu Val Val Val Pro Ile Val
130 135 140

Ser Arg Glu Thr Cys Arg Ser Ala Tyr Gly Gly Thr Val Thr Asp Thr
145 150 155 160

Met Ile Cys Ala Gly Ala Leu Gly Gly Lys Asp Ala Cys Gln Gly Asp
165 170 175

Ser Gly Gly Pro Leu Val Cys Ser Asp Gly Glu Leu Val Gly Ile Val
180 185 190

Ser Trp Gly Tyr Gly Cys Ala Val Gly Asn Tyr Pro Gly Val Tyr Thr
195 200 205

Arg Val Ser Arg Tyr Leu Asp Trp Ile
210 215

<210> 89

<211> 79

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Divergent
subfamily of APPLE domains Consensus Sequence

<400> 89

Lys Ser Asp Asp Cys Phe Val Arg Leu Pro Asn Thr Lys Leu Pro Asp
1 5 10 15

Phe Ser Pro Ile Val Ile Ser Val Ala Ser Leu Glu Glu Cys Ala Gln
20 25 30

Lys Cys Leu Asn Ser Asn Cys Ser Cys Arg Ser Phe Thr Tyr Asn Asn
35 40 45

Asp Thr Lys Gly Cys Leu Leu Trp Ser Glu Ser Ser Leu Gly Asp Ala
50 55 60

Arg Gln Leu Leu Pro Ser Gly Gly Val Asp Tyr Tyr Glu Lys Ile
65 70 75

<210> 90

<211> 145

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Lipocalin/cytosolic fatty-acid binding protein
family Consensus Sequence

<400> 90

Lys Phe Ala Gly Lys Trp Tyr Leu Val Ala Ser Ala Asn Phe Asp Pro
1 5 10 15

Glu Leu Lys Glu Glu Leu Gly Val Leu Glu Ala Thr Arg Lys Glu Ile
20 25 30

Thr Pro Leu Lys Glu Gly Asn Leu Glu Ile Val Phe Asp Gly Asp Lys
35 40 45

Asn Gly Ile Cys Glu Glu Thr Phe Gly Lys Leu Glu Lys Thr Lys Lys
50 55 60

Leu Gly Val Glu Phe Asp Tyr Tyr Thr Gly Asp Asn Arg Phe Val Val
65 70 75 80

Leu Asp Thr Asp Tyr Asp Asn Tyr Leu Leu Val Cys Val Gln Lys Gly
85 90 95

Asp Gly Asn Glu Thr Ser Arg Thr Ala Glu Leu Tyr Gly Arg Thr Pro
100 105 110

Glu Leu Ser Pro Glu Ala Leu Glu Leu Phe Glu Thr Ala Thr Lys Glu
115 120 125

Leu Gly Ile Pro Glu Asp Asn Val Val Cys Thr Arg Gln Thr Glu Arg
130 135 140

Cys

145

<210> 91
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Connexin
 Consensus Sequence

<400> 91
 Met Asp Trp Ser Phe Leu Gly Arg Leu Leu Glu Gly Val Asn Lys His
 1 5 10 15
 Ser Thr Ala Ile Gly Lys Ile Trp Leu Ser Val Leu Phe Ile Phe Arg
 20 25 30
 Ile Leu Val Leu Gly Val Ala Ala Glu Ser Val Trp Gly Asp Glu Gln
 35 40 45
 Ser Asp Phe Val Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val Cys
 50 55 60
 Tyr Asp Gln Phe Phe Pro Ile Ser His Val Arg Leu Trp Val Leu Gln
 65 70 75 80
 Leu Ile Phe Val Ser Thr Pro Ser Leu Leu Tyr Leu Gly His Val Ala
 85 90 95
 Tyr Arg Val Arg Arg Glu Glu Lys Leu Arg Glu Lys Glu Glu Glu His
 100 105 110
 Ser Lys Gly Leu Tyr Ser Glu Glu Ala Lys Lys Arg Cys Gly Ser Glu
 115 120 125
 Asp Gly Lys Val Arg Ile Arg Gly Gly Leu Trp Trp Thr Tyr Val Phe
 130 135 140
 Ser Ile Ile Phe Lys Ser Ile Phe Glu Val Gly Phe Leu Tyr Gly Gln
 145 150 155 160
 Tyr Leu Leu Tyr Gly Phe Thr Met Ser Pro Leu Val Val Cys Ser Arg
 165 170 175
 Ala Pro Cys Pro His Thr Val Asp Cys Phe Val Ser Arg Pro Thr Glu
 180 185 190
 Lys Thr Ile Phe Ile Val Phe Met Leu Val Val Ser Ala Ile Cys Leu
 195 200 205
 Leu Leu Asn Leu Ala Glu Leu Phe Tyr Leu
 210 215

<210> 92
 <211> 59

<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Src homology 3
domains Consensus Sequence

<400> 92

Glu Gly Pro Gln Val Arg Ala Leu Tyr Asp Tyr Thr Ala Gln Asp Pro
1 5 10 15

Asp Glu Leu Ser Phe Lys Lys Gly Asp Ile Ile Thr Val Leu Glu Lys
20 25 30

Ser Asp Asp Gly Trp Trp Lys Gly Arg Leu Gly Thr Gly Lys Glu Gly
35 40 45

Leu Phe Pro Ser Asn Tyr Val Glu Glu Ile Asp
50 55

<210> 93

<211> 57

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SH3 domain
Consensus Sequence

<400> 93

Pro Lys Val Val Ala Leu Tyr Asp Tyr Gln Ala Arg Glu Ser Asp Glu
1 5 10 15

Leu Ser Phe Lys Lys Gly Asp Ile Ile Ile Val Leu Glu Lys Ser Asp
20 25 30

Asp Gly Gly Trp Trp Lys Gly Arg Leu Lys Gly Thr Lys Glu Gly Leu
35 40 45

Ile Pro Ser Asn Tyr Val Glu Pro Val
50 55

<210> 94

<211> 91

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fes/CIP4
homology domain Consensus Sequence

<400> 94

Met Gly Phe Trp Ser Glu Leu Asp Asp Gly Phe Glu Ala Leu Leu Ser
1 5 10 15

Arg Leu Lys Asn Gly Leu Arg Leu Leu Glu Asp Leu Lys Lys Phe Met
20 25 30

Arg Glu Arg Ala Lys Ile Glu Glu Glu Tyr Ala Lys Lys Leu Gln Lys
35 40 45

Leu Ser Lys Lys Leu Arg Ala Val Arg Asp Thr Glu Ser Glu Leu Gly
50 55 60

Ser Leu Arg Lys Ala Trp Glu Val Leu Leu Ser Glu Thr Asp Ala Leu
65 70 75 80

Ala Lys Gln His Leu Gln Leu Ser Glu Asp Leu
85 90

<210> 95

<211> 94

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fes/CIP4
homology domain Consensus Sequence

<400> 95

Met Gly Phe Gly Ser Glu Leu Cys Pro Glu Gly His Lys Ala Leu Leu
1 5 10 15

Ser Arg Gln Asp Asn Glu Leu Arg Leu Leu Glu Glu Met Lys Lys Phe
20 25 30

Met Ala Glu Arg Ala Lys Ile Glu Lys Glu Tyr Ala Gly Lys Leu Gln
35 40 45

His Leu Ser Ala Gln Val Gly Lys Gly Pro Ala Thr Ala Glu Gly Glu
50 55 60

Asp Glu Leu Ser Ser Leu Lys Ser Trp Ala Val Ile Leu Ser Glu Thr
65 70 75 80

Glu Gln Gln Ser Lys Ile His Leu Gln Ile Ser Glu Asp Leu
85 90

<210> 96

<211> 230

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Trypsin-like
serine protease Consensus Sequence

<400> 96

Arg Ile Val Gly Gly Ser Glu Ala Asn Ile Gly Ser Phe Pro Trp Gln
1 5 10 15

Val Ser Leu Gln Tyr Arg Gly Gly Arg His Phe Cys Gly Gly Ser Leu
 20 25 30
 Ile Ser Pro Arg Trp Val Leu Thr Ala Ala His Cys Val Tyr Gly Ser
 35 40 45
 Ala Pro Ser Ser Ile Arg Val Arg Leu Gly Ser His Asp Leu Ser Ser
 50 55 60
 Gly Glu Glu Thr Gln Thr Val Lys Val Ser Lys Val Ile Val His Pro
 65 70 75 80
 Asn Tyr Asn Pro Ser Thr Tyr Asp Asn Asp Ile Ala Leu Leu Lys Leu
 85 90 95
 Ser Glu Pro Val Thr Leu Ser Asp Thr Val Arg Pro Ile Cys Leu Pro
 100 105 110
 Ser Ser Gly Tyr Asn Val Pro Ala Gly Thr Thr Cys Thr Val Ser Gly
 115 120 125
 Trp Gly Arg Thr Ser Glu Ser Ser Gly Ser Leu Pro Asp Thr Leu Gln
 130 135 140
 Glu Val Asn Val Pro Ile Val Ser Asn Ala Thr Cys Arg Arg Ala Tyr
 145 150 155 160
 Ser Gly Gly Pro Ala Ile Thr Asp Asn Met Leu Cys Ala Gly Gly Leu
 165 170 175
 Glu Gly Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
 180 185 190
 Cys Asn Asp Pro Arg Trp Val Leu Val Gly Ile Val Ser Trp Gly Ser
 195 200 205
 Tyr Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Thr Arg Val Ser
 210 215 220
 Ser Tyr Leu Asp Trp Ile
 225 230

<210> 97

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Trypsin
 Consensus Sequence

<400> 97

Ile Val Gly Gly Arg Glu Ala Gln Ala Gly Ser Phe Pro Trp Gln Val
 1 5 10 15

Ser Leu Gln Val Ser Ser Gly His Phe Cys Gly Gly Ser Leu Ile Ser
 20 25 30
 Glu Asn Trp Val Leu Thr Ala Ala His Cys Val Ser Gly Ala Ser Ser
 35 40 45
 Val Arg Val Val Leu Gly Glu His Asn Leu Gly Thr Thr Glu Gly Thr
 50 55 60
 Glu Gln Lys Phe Asp Val Lys Lys Ile Ile Val His Pro Asn Tyr Asn
 55 70 75 80
 Pro Asp Thr Asn Asp Ile Ala Leu Leu Lys Leu Lys Ser Pro Val Thr
 85 90 95
 Leu Gly Asp Thr Val Arg Pro Ile Cys Leu Pro Ser Ala Ser Ser Asp
 100 105 110
 Leu Pro Val Gly Thr Thr Cys Ser Val Ser Gly Trp Gly Arg Thr Lys
 115 120 125
 Asn Leu Gly Thr Ser Asp Thr Leu Gln Glu Val Val Val Pro Ile Val
 130 135 140
 Ser Arg Glu Thr Cys Arg Ser Ala Tyr Gly Gly Thr Val Thr Asp Thr
 145 150 155 160
 Met Ile Cys Ala Gly Ala Leu Gly Gly Lys Asp Ala Cys Gln Gly Asp
 165 170 175
 Ser Gly Gly Pro Leu Val Cys Ser Asp Gly Glu Leu Val Gly Ile Val
 180 185 190
 Ser Trp Gly Tyr Gly Cys Ala Val Gly Asn Tyr Pro Gly Val Tyr Thr
 195 200 205
 Arg Val Ser Arg Tyr Leu Asp Trp Ile
 210 215

<210> 98

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: NOV5 Primer 1

<400> 98

ctccactcc tgcgtcttct gact

24

<210> 99

<211> 25

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: NOV5 Primer 2

 <400> 99
 aaggctgggc ctaaccagc ctcac 25

 <210> 100
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV7 Primer 1

 <400> 100
 catgaactgg gcatttctgc agg 23

 <210> 101
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV7 Primer 2

 <400> 101
 ttatctgctg atctcgcagg ttatgga 27

 <210> 102
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV8 Primer 1

 <400> 102
 ctgacaggcc ctggtgtgtg at 22

 <210> 103
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV8 Primer 2

 <400> 103
 tcacacatgt ttcattgtggg agttaga 27

 <210> 104
 <211> 24

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV9 Primer 1

 <400> 104
 gagtgagagg tcggacagac tgtg 24

 <210> 105
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV9 Primer 2

 <400> 105
 actcatgcaa cttgcttctc tcactct 27

 <210> 106
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV10b Primer
 1

 <400> 106
 cctatgagcc tgatgctgga tgac 24

 <210> 107
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV10b Primer
 2

 <400> 107
 aggactcaga ggagggagtc ctgag 25

 <210> 108
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag4164 Forward

 <400> 108

gcactacaag tggaagcctt ac 22

<210> 109
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag4164 Probe

<400> 109
ctcaagtaga agccgactta tgcaaa 26

<210> 110
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag4164 Reverse

<400> 110
tcaaattcctt ctgcatata gt 22

<210> 111
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag1313b
Forward

<400> 111
cagctgcacg attaatgaag at 22

<210> 112
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag1313b Probe

<400> 112
aggtcttggg ctggccttca ccatt 25

<210> 113
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag1313b
 Reverse

<400> 113
 ccaaagttgt gtccagactc at 22

<210> 114
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag2197 Forward

<400> 114
 ccaaggaaga cctcttcac tt 22

<210> 115
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag2197 Probe

<400> 115
 tcttgcttac ggcataagcg ctctct 26

<210> 116
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag2197 Reverse

<400> 116
 ttcatttcta tgggacctca ga 22

<210> 117
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag708 Forward

<400> 117
 aaagatggga ctcgtcatga c 21

<210> 118

<211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag708 Probe

 <400> 118
 cacgccatct tactgactgg tctgga 26

 <210> 119
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag708 Reverse

 <400> 119
 gtgcaaattcc caaagtgtca 20

 <210> 120
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag4164 Forward

 <400> 120
 gcactacaag tggaagcctt ac 22

 <210> 121
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag4164 Probe

 <400> 121
 ctcaagtaga agccgactta tgcaaa 26

 <210> 122
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag4164 Reverse

 <400> 122
 tcaaattcctt ctgcgatata gt 22

<210> 123
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag2197 Forward

<400> 123
ccaaggaaga cctcttcac tt 22

<210> 124
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag2197 Probe

<400> 124
tcttgcttac ggcataagcg ctctct 26

<210> 125
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag2197 Reverse

<400> 125
ttcatttcta tgggacctca ga 22

<210> 126
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag2197 Forward

<400> 126
ccaaggaaga cctcttcac tt 22

<210> 127
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag2197 Probe

<400> 127
tcttgcttac ggcataagcg ctctct 26

<210> 128
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag2197 Reverse

<400> 128
ttcatttcta tgggacctca ga 22

<210> 129
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag708 Forward

<400> 129
aaagatggga ctcgcatga c 21

<210> 130
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag708 Probe

<400> 130
cacgccatct tactgactgg tctgga 26

<210> 131
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag708 Reverse

<400> 131
gtgcaaattcc caaagtgtca 20

<210> 132
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag1313b
 Forward

<400> 132
 cagctgcacg attaatgaag at 22

<210> 133
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag1313b Probe

<400> 133
 aggtcttgga ctggccttca ccatt 25

<210> 134
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag1313b
 Reverse

<400> 134
 ccaaagttgt gtccagactc at 22

<210> 135
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag1537 Forward

<400> 135
 tttcaagaca ccctgtgata cc 22

<210> 136
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag1537 Probe

<400> 136
 acttcgtgtc ctgaatgttc cagget 26

<210> 137
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag1537 Reverse

 <400> 137
 cagaggaatg aaggcataga tg 22

 <210> 138
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2432 Forward

 <400> 138
 gtaggcaaag ggactcactg t 21

 <210> 139
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2432 Probe

 <400> 139
 cagaaatcaa taatctttga ctgcog 26

 <210> 140
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2432 Reverse

 <400> 140
 gcacattacg tggctgaga 19

 <210> 141
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag1250 Forward

<400> 141
cgtggtgaac tctgccttat at 22

<210> 142
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag1250 Probe

<400> 142
cacagagctg tcgtctttga ccgatt 26

<210> 143
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag1250 Reverse

<400> 143
agtccctttg cctaccacaa t 21

<210> 144
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag3086 Forward

<400> 144
ggacccatt cgactactgt 20

<210> 145
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag3086 Probe

<400> 145
ctgatgacca gccgccatca atc 23

<210> 146
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag3086 Reverse

 <400> 146
 ttctcaaact gcacctggtc 20

 <210> 147
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag3797 Forward

 <400> 147
 tctggacgac aactattgcc 20

 <210> 148
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag3797 Probe

 <400> 148
 atggtgctac actacggatc cgcag 25

 <210> 149
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag3797 Reverse

 <400> 149
 gtcacagaat tctcgctcga 20

 <210> 150
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2439 Forward

 <400> 150
 tatcatcact tgtgatggca aa 22

 <210> 151
 <211> 26

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2439 Probe

 <400> 151
 aaaaccgaga gcactttgaa aacaca 26

 <210> 152
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2439 Reverse

 <400> 152
 aaacttctct cccagggtag aa 22

 <210> 153
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2771 Forward

 <400> 153
 tgaacagaac tatgcgaaac aa 22

 <210> 154
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2771 Probe

 <400> 154
 tctgggtaag aagtactgcc ccaaacg 27

 <210> 155
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2771 Reverse

 <400> 155
 ggctcttcat ctttggatga a 21

<210> 156
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag1674 Forward

<400> 156
ctcactcacc acaagggagt aa 22

<210> 157
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag1674 Probe

<400> 157
tgacatcaaa ctcaacagtt cccagga 27

<210> 158
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag1674 Reverse

<400> 158
gtctaggaga gagctgagca aa 22

<210> 159
<211> 78
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PAN domain
Consensus Sequence

<400> 159
Cys Ser Ser Phe Val Arg Val Pro Gly Arg Ser Leu Ser Gly Asn Asp
1 5 10 15

Ile Ser Val Val Asn Val Pro Ser Leu Glu Glu Cys Ala Ala Leu Cys
20 25 30

Leu Glu Glu Pro Arg Val Cys Arg Ser Phe Thr Tyr Asn Asn Lys Ser
35 40 45

Lys Gln Cys Leu Leu Lys Ser Glu Ser Ser Gly Ser Leu Pro Arg Leu

50

55

60

Lys Arg Pro Ser Gln Lys Val Asp Tyr Tyr Glu Lys Ser Cys
 65 70 75

<210> 160

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Connexin
 homologues Consensus Sequence

<400> 160

Ser Val Trp Gly Asp Glu Gln Ser Asp Phe Thr Cys Asn Thr Gln Gln
 1 5 10 15

Pro Gly Cys Glu Asn Val Cys Tyr Asp Gln Phe Phe Pro Ile Ser His
 20 25 30

Val Arg